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OM protein - protein search, using sw model

Run on: April 19, 2004, 13:16:02; Search time 38.2387 Seconds

(without alignments)

1359.585 Million cell updates/sec

Title: PCT-US03-05147-1

Perfect score: 964

Sequence: 1 MLQMAGQCSQNEYFDSLLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Query				
No.	Score	Match	Length	DB	ID	Description
1	964	100.0	184	3	AAB08843	Aab08843 Amino aci
2	964	100.0	184	3	AAY94001	Aay94001 A human B
3	964	100.0	184	4	AAE09241	Aae09241 Human BCM
4	964	100.0	184	4	AAY71979	Aay71979 Human B c
5	964	100.0	184	4	AAB60698	Aab60698 Human BAF
6	964	100.0	184	4	AAE00506	Aae00506 Human B c
7	964	100.0	184	5	ABB81487	Abb81487 Human BCM
8	964	100.0	184	5	ABP54694	Abp54694 Metastati
9	964	100.0	184	5	AAE28961	Aae28961 Human B-c

1.0	0.64	100 0	101	_	7 7 TO 2 C 0 1 C	725216 H D	_
10	964	100.0	184	6	AAE35216	Aae35216 Human B	
11	964	100.0	184	6	ADA49361	Ada49361 Human Bo	
12	964	100.0	184	6	ABP60552	Abp60552 Human to	
13	964	100.0	184	6	ABP97717	Abp97717 Amino a	
14	964	100.0	184	7	ADD67527	Add67527 Human L	
15	958	99.4	184	6	ABR40082	Abr40082 Human Ge	
16	955	99.1	288	5	ABG95060	Abg95060 Human t	
17	950	98.5	181	5	AAE15484	Aae15484 Human B	
18	719.5	74.6	157	4	AAB60700	Aab60700 Human B	
19	572	59.3	185	3	AAB08844	Aab08844 Amino a	ci
20	572	59.3	185	4	AAY71980	Aay71980 Murine l	В
21	572	59.3	185	5	AAE15490	Aae15490 Mouse B	С
22	323	33.5	58	5	AAE15501	Aae15501 Human B	С
23	311.5	32.3	117	5	AAE15491	Aae15491 Human-m	ur
24	286.5	29.7	302	4	AAB60699	Aab60699 Mouse I	gG
25	286.5	29.7	302	4	AAE00507	Aae00507 Human B	CM
26	286	29.7	283	5	AAE15488	Aae15488 Human B	СМ
27	284	29.5	51	5	AAE15485	Aae15485 Human B	-c
28	201	20.9	34	5	AAE15486	Aae15486 Human B-	-c
29	201	20.9	34	6	ADA49366	Ada49366 Human B	СМ
30	187	19.4	281	5	AAE15489	Aae15489 Mouse B	СМ
31	158	16.4	42	6	ABJ38417	Abj38417 TALL-1	re
32	116.5	12.1	175	5	ABB78398	Abb78398 Amino ao	ci
33	116.5	12.1	175	5	AAE22244	Aae22244 Murine 1	BA
34	116.5	12.1	175	5	ABB81489	Abb81489 Mouse Zi	tn
35	116.5	12.1	175	6	ABP97722	Abp97722 Amino ao	
36	106.5	11.0	185	5	AAE22266	Aae22266 Human Bi	
37	105.5	10.9	185	5	AAE22267	Aae22267 Human B	
38	104	10.8	21	5	AAE15487	Aae15487 Human B	-c
39	103.5	10.7	185	5	AAE22269	Aae22269 Human B	AF
40	100.5	10.4	185	5	AAE22271	Aae22271 Human Bi	AF
41	100	10.4	185	7	ADB90663	Adb90663 TALL-1R	
42	99.5	10.3	185	5	AAE22268	Aae22268 Human B	_
43	97.5	10.1	185	5	AAE22270	Aae22270 Human Bi	
44	94.5	9.8	185	5	AAE22242	Aae22242 Human ma	
45	93	9.6	184	5	ABB81483	Abb81483 Human Z	
1 5	, ,	5.0	101	_		I DE SEL TOUR HUMANI D	

ALIGNMENTS

```
RESULT 1
    AAB08843 standard; peptide; 184 AA.
ID
XX
    AAB08843;
AC
XX
DT
    02-JAN-2001 (first entry)
XX
DE
    Amino acid sequence of human.
XX
     BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
K₩
     anti-cell death gene; apoptosis; viral infection; inflammatory response;
KW
     rheumatoid arthritis; inflammatory bowel disease; septic shock.
KW
XX
     Homo sapiens.
OS
XX
```

```
FH
     Key
                    Location/Qualifiers
FT
     Domain
                    57. .77
FT
                    /note= "putative transmembrane domain"
XX
PN
    W0200050633-A1.
XX
PD
    31-AUG-2000.
XX
    24-FEB-2000; 2000WO-US004925.
ΡF
XX
    24-FEB-1999;
                   99US-0121485P.
PR
XX
PΑ
     (GEHO ) GEN HOSPITAL CORP.
XX
PΙ
    Seed B, Ting A;
XX
    WPI; 2000-558405/51.
DR
XX
PT
    Identifying a modulator of gene expression for drug designing, by
РΤ
    contacting a compound library with a cell expressing an anti-cell death
PT
    gene and reporter gene, and determining alteration in reporter gene
PT
    expression.
XX
PS
    Claim 32; Fig 7A; 53pp; English.
XX
CC
    The present sequence represents a BCMA (not defined) polypeptide. BCMA is
CC
    a necrosis factor (NF)-kB activator. The method of the invention is used
    to identify compounds which modulate BCMA activity (and thus NF-kB
CC
CC
    activity). The specification describes a method of identifying a
CC
    polypeptide which increases gene expression from a promoter. The method
CC
    involves contacting a library of with a cell which expresses a
CC
    recombinant anti-cell death gene and a reporter gene operably linked to
CC
    the promoter, and then determining whether the expression of the reporter
CC
    gene is altered as a result of contact with library. The method is useful
CC
    for identifying polypeptides which increase or decrease gene expression
CC
    from a promoter. The BCMA polypeptide or nucleic acid are useful for
CC
    preparing a pharmaceutical composition for treating cancer, apoptosis,
CC
    viral infections, inflammatory response, such as rheumatoid arthritis,
    inflammatory bowel disease or septic shock. BCMA is useful for
CC
    identifying compounds that modulate NF-kB expression and thus for drug
CC
CC
    designing
XX
SQ
    Sequence 184 AA;
                        100.0%; Score 964; DB 3; Length 184;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches
                                               0;
                                                   Indels
                                                              0; Gaps
                                                                         0:
QУ
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             Db
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Qy
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         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy
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121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db
          181 ISAR 184
Qу
              Db
          181 ISAR 184
RESULT 2
AAY94001
ΙD
     AAY94001 standard; protein; 184 AA.
XX
AC
     AAY94001;
XX
DT
     20-OCT-2000 (first entry)
XX
DE
     A human BCMA protein, a B cell protein related to TACI.
XX
KW
     Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KW
     transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
KW
     ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
     systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KW
     rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
KW
     end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KW
     renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
KW
     immune response; immunosuppression; graft rejection; joint pain;
KW
     graft versus host disease; inflammation; swelling; anaemia; septic shock;
KW
     insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KW
     renal artery stenosis; occlusion; cholesterol; renal emboli.
XX
OS
    Homo sapiens.
XX
    W0200040716-A2.
PN
XX
PD
     13-JUL-2000.
XX
ΡF
     07-JAN-2000; 2000WO-US000396.
XX
PR
     07-JAN-1999;
                   99US-00226533.
XX
PΑ
     (ZYMO ) ZYMOGENETICS INC.
XX
PΙ
     Gross JA, Xu W, Madden K, Yee DP;
XX
     WPI; 2000-452538/39.
DR
    N-PSDB; AAA58559.
DR
XX
PT
     Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
РΤ
     renal disease, graft versus host disease, and inflammation, comprises
PT
     administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
XX
PS
     Disclosure; Page 152; 175pp; English.
XX
     The present sequence represents a human BCMA protein, a B cell protein
CC
CC
     related to transmembrane activator and CAML-interactor (TACI) receptor.
CC
     TACI is a tumour necrosis factor (TNF) receptor. The extracellular
CC
     domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
```

```
CC
     protein) receptor contain a cysteine rich domain, and are used for
     inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used
CC
     for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
CC
CC
     with activated or resting B lymphocytes, effector T-cells, or with
CC
     antibody production. The antibody production is associated with an
     autoimmune disease selected from systemic lupus erythematosus, myasthenia
CC
     gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity
CC
CC
     and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
CC
     asthma, bronchitis, emphysema, end stage renal failure,
CC
     glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal
CC
     neoplasms, multiple myelomas, lymphomas, light chain neuropathy,
CC
     amyloidosis, moderating immune response, immunosuppression, graft
CC
     rejection, graft versus host disease, inflammation, insulin dependent
CC
     diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
CC
     septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
     agonists or antagonists can be used to treat hypertension, renal artery
CC
CC
     stenosis, or occlusion, and cholesterol or renal emboli
XX
SO
     Sequence 184 AA;
  Query Match
                        100.0%; Score 964; DB 3;
                                                  Length 184;
  Best Local Similarity
                        100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative
                             0; Mismatches
                                               0; Indels
                                                            0; Gaps
                                                                        0;
Qу
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
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           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
             Db
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         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
             121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db
         181 ISAR 184
Qу
             Db
         181 ISAR 184
RESULT 3
AAE09241
    AAE09241 standard; protein; 184 AA.
XX
AC
    AAE09241;
XX
DT
    19-NOV-2001 (first entry)
XX
DΕ
    Human BCMA protein.
XX
KW
    Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
    TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW
KW
    autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX
OS
    Homo sapiens.
XX
```

```
PN
     W0200160397-A1.
XX
PD
     23-AUG-2001.
XX
PF
     28-NOV-2000; 2000WO-US032378.
XX
PR
     16-FEB-2000; 2000US-0182938P.
PR
     22-AUG-2000; 2000US-0226986P.
XX
PA
     (GETH ) GENENTECH INC.
XX
PΙ
    Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
PΙ
    Yan M:
XX
    WPI; 2001-541628/60.
DR
    N-PSDB; AAD15902.
DR
XX
РΤ
    Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT
    activity, for treating autoimmune disorders and cancer, comprises
PT
    exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT
    antagonists.
XX
PS
    Example 2; Fig 2; 160pp; English.
XX
CC
    The invention relates to methods of using one or more agonists or
CC
    antagonists to modulate the activity of the members of TNF (tumour
CC
    necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
CC
    TACI or BCMA. The method is useful for treating pathological conditions
CC
    or diseases associated with increased TALL-1 and APRIL expression or
CC
    activity. TALL-1 and APRIL antagonists are used to block the interaction
CC
    between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
CC
    a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
CC
    cancers of lung and colon and autoimmune diseases e.g. rheumatoid
CC
    arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
    present sequence is human BCMA protein
CC
XX
SO
    Sequence 184 AA;
 Query Match
                       100.0%; Score 964; DB 4; Length 184;
 Best Local Similarity 100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative 0; Mismatches 0; Indels
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Qу
             Db
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Qу
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          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Db
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QУ
             121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db
         181 ISAR 184
Qу
            1111
Db
         181 ISAR 184
```

```
RESULT 4
AAY71979
     AAY71979 standard; protein; 184 AA.
XX
AC
     AAY71979;
XX
DT
     28-MAR-2001
                 (first entry)
XX
DE
     Human B cell maturation factor (BCMA) protein.
XX
KW
     Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
KW
     Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1;
KW
     therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
     systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
KW
     thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
KW
KW
     haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;
KW
     post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
KW
     B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
XX
OS
     Homo sapiens.
XX
FH
     Key
                     Location/Qualifiers
FT
     Domain
                     1. .62
FT
                     /label= Extracellular domain
XX
ΡN
     W0200068378-A1.
XX
PD
     16-NOV-2000.
XX
PF
     05-MAY-2000; 2000WO-US012266.
XX
PR
     06-MAY-1999;
                    99US-0132892P.
PR
     01-MAY-2000; 2000US-0201012P.
XX
PΑ
     (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
PΙ
     Shu HS;
XX
DR
    WPI; 2001-016094/02.
DR
    N-PSDB; AAD02125.
XX
PT
     Isolated TALL-1 protein is used to identify compounds that regulate B
     lymphocyte proliferation, used to treat B lymphocyte associated
PT
PT
     autoimmune disorders.
XX
PS
    Claim 37; Page 104-105; 112pp; English.
XX
CC
    The present invention relates to Tumour necrosis factor (TNF) and ApoL-
     related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
CC
CC
    proteins (including homologues), and their antibodies. The invention in
    particular relates to methods for regulating the interaction between TALL
CC
CC
    -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
CC
     regulate monocyte, macrophage and B lymphocyte mediated immune responses.
    TALL-1 protein is useful for identifying compounds that regulate B
CC
CC
    lymphocyte proliferation. It is also useful for treating B lymphocyte
```

```
associated autoimmune disorders like rheumatoid arthritis, systemic lupus
CC.
     erythematosus (SLE), insulin dependent diabetes mellitus, multiple
CC
CC
     sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
     anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
CC
CC
     pemphigus vulgaris, acute rheumatic fever, post-streptococcal
CC
     glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
CC
     corresponding nucleic acid sequence are also useful in diagnostic assays.
CC
     The present sequence is a human B cell maturation factor (BCMA) protein.
     It is the receptor for TALL-1 protein. BCMA gene is located on chromosome
CC
CC
     16. In human tissues, BCMA is expressed by spleen and lymph nodes but not
CC
     by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.
     BCMA mRNA is absent in the pro-B lymphocyte stage but its expression
CC
CC
     increases with B lymphocyte maturation
XX
SO
     Sequence 184 AA;
  Query Match
                        100.0%; Score 964; DB 4;
                                                  Length 184;
  Best Local Similarity
                        100.0%; Pred. No. 7.6e-95;
  Matches 184; Conservative 0; Mismatches
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                                                             0;
                                                                 Gaps
                                                                        0;
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
QУ
             Db
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Qу
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Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QУ
             Db
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         181 ISAR 184
Qу
             Db
         181 ISAR 184
RESULT 5
AAB60698
ΙD
    AAB60698 standard; protein; 184 AA.
XX
AC
    AAB60698;
XX
DT
    22-MAY-2001 (first entry)
XX
DΕ
    Human BAFF receptor (BAFF-R).
XX
    Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
KW
KW
    immune-related disorder; B-cell growth inhibitor; BCMA;
KW
    B-cell maturation inhibitor; immunoglobulin production inhibitor;
KW
    autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
KW
    renal disorder; immunosuppressive disorder; HIV infection;
    organ transplantation; antiinflammatory; systemic lupus erythematosus;
KW
    autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;
KW
    B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
KW
KW
    lymphoma; gene therapy; cancer; tumour.
XX
```

```
OS
     Homo sapiens.
XX
ΡN
     WO200112812-A2.
XX
     22-FEB-2001.
PD
XX
PF
     16-AUG-2000; 2000WO-US022507.
XX
PR
     17-AUG-1999;
                    99US-0149378P.
PR
     11-FEB-2000; 2000US-0181684P.
     18-FEB-2000; 2000US-0183536P.
PR
XX
PΑ
     (BIOJ ) BIOGEN INC.
PΑ
     (APOT-) APOTECH R & D SA.
XX
PΙ
     Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;
     Thompson J;
PΙ
XX
DR
     WPI; 2001-202866/20.
DR
     N-PSDB; AAF59998.
XX
PT
     Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
PT
     lympho-proliferative disorder by administering BAFF-receptor polypeptide,
PT
     chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
XX
PS
     Claim 20; Fig 1; 59pp; English.
XX
CC
     The invention relates to the use of a BAFF receptor (BAFF-R, also known
CC
     as BCMA) protein, or a BAFF-R fusion protein as an agent for the
     treatment of a variety of immune-related disorders. BAFF-R is a member of
CC
     the TNF (tumour necrosis factor) family, acting as an immunoregulatory
CC
CC
     agent, and also plays a role in the development of hypertension and
CC
     related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-
CC
     specific antibodies can be used for inhibiting B-cell growth, dendritic
     cell-induced B-cell growth and maturation, and immunoglobulin production,
CC
CC
     and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC
     disorders, hypertension and renal disorders. The BAFF-R proteins may also
CC
     be used in the treatment of immunosuppressive disorders and HIV
CC
     infection, and in patients undergoing organ transplantation. The BAFF-R
CC
     proteins or BAFF-R specific antibodies may be used for treating,
     suppressing or altering an immune response involving a signalling pathway
CC
CC
     between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
CC
     inhibits B-cell growth and maturation it is useful for treating diseases
     such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
CC
CC
     Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
CC
    progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
CC
    human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
     autoimmune disorders and inherited B-cell-associated disorders. The
CC
CC
    present sequence represents human BAFF-R
XX
SQ
     Sequence 184 AA;
  Query Match
                          100.0%; Score 964; DB 4; Length 184;
 Best Local Similarity
                         100.0%; Pred. No. 7.6e-95;
 Matches 184; Conservative
                               0; Mismatches
                                                  0; Indels
                                                                     Gaps
                                                                             0;
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QУ

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Db
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Qу
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
             61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Db
QУ
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATETEKS 180
             Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
         181 ISAR 184
Qv
             Db
         181 ISAR 184
RESULT 6
AAE00506
ID
    AAE00506 standard; protein; 184 AA.
XX
AC
    AAE00506;
XX
DT
    31-JUL-2001 (first entry)
XX
DE
    Human B cell maturation protein (BCMA).
XX
KW
    Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
    gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW
KW
    carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW
    systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW
    B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
    organ transplantation; HIV; human immunodeficiency virus; TNF;
KW
KW
    tumour necrosis factor; BCMA; B cell maturation protein.
XX
OS
    Homo sapiens.
XX
PN
    W0200124811-A1.
XX
PD
    12-APR-2001.
XX
    05-OCT-2000; 2000WO-US027579.
PF
XX
PR
    06-OCT-1999;
                  99US-0157933P.
    11-FEB-2000; 2000US-0181807P.
PR
PR
    30-JUN-2000; 2000US-0215688P.
XX
PA
    (BIOJ ) BIOGEN INC.
    (APOT-) APOTECH R & D SA.
PA
XX
PΙ
    Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;
XX
DR
    WPI; 2001-266242/27.
DR
    N-PSDB; AAD03844.
XX
PT
    Treating a mammal for a condition associated with undesired cell
PΤ
    proliferation such as cancer or carcinoma, comprises administering a
PΤ
    composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
```

```
PT
     antagonist.
XX
PS
     Claim 3; Fig 3A; 85pp; English.
XX
     The invention relates to a method of treating a mammal for a condition
CC
     associated with undesired cell proliferation such as cancer or carcinoma.
CC
CC
     The method involves administering a composition comprising A
CC
     Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell
     maturation protein (BCM or BCMA) antagonist that antagonises the
CC
     interaction between APRIL and its cognate receptor(s). This method is
CC
CC
     useful for treating undesired cell proliferation such as cancer or
CC
     carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
CC
     prostate carcinoma, and other carcinomas whose proliferation is modulated
CC
     by APRIL. It is also useful for treating autoimmune diseases (Grave's
CC
     disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
     diseases, renal disorders, B-cell lympho-proliferative disorders,
CC
     immunosuppressive diseases, organ transplantation, inflammation and human
CC
CC
     immunodeficiency virus (HIV), and for treating, suppressing or altering
CC
     an immune response involving a signalling pathway between APRIL-R and its
CC
     ligand. APRIL-R DNA is also useful in gene therapy. The present sequence
CC
    is human APRIL-R also referred as BCMA or BCM protein
XX
SQ
    Sequence 184 AA;
                        100.0%; Score 964; DB 4; Length 184; 100.0%; Pred. No. 7.6e-95;
  Query Match
  Best Local Similarity
 Matches 184; Conservative
                             0; Mismatches
                                               0; Indels
                                                             0; Gaps
                                                                         0:
QУ
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCL 60
             Db
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
QУ
             61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qv
             Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
         181 ISAR 184
Qу
             1111
Db
         181 ISAR 184
RESULT 7
ABB81487
    ABB81487 standard; protein; 184 AA.
XX
AC
    ABB81487;
XX
    02-SEP-2002 (first entry)
DT
XX
DE
    Human BCMA receptor related protein SEQ ID NO:7.
XX
KW
    Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
KW
    immunosuppressive; dermatological; antiinflammatory; antidiabetic;
```

KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic; KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; KW KW multiple sclerosis; insulin dependent diabetes mellitus; asthma; KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis; KW light chain neuropathy; hypertension; large vessel disease; KW graft-versus host disease; graft rejection; Crohn's disease. XX OS Homo sapiens. XX PN W0200238766-A2. XX PD 16-MAY-2002. XX PF05-NOV-2001; 2001WO-US047018. XX PR 07-NOV-2000; 2000US-0246449P. PR 20-DEC-2000; 2000US-0257131P. PR 28-JUN-2001; 2001US-0301715P. PR 29-AUG-2001; 2001US-0315565P. XX PΑ (ZYMO) ZYMOGENETICS INC. XX PΙ Gross JA, Xu W, Henne RM, Grant FJ; XX DR WPI; 2002-508212/54. XX PΤ Novel isolated human tumor necrosis factor receptor polypeptide, termed Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage PTPΤ renal failure or renal disease and lymphoma. XX PS Disclosure; Page 135-136; 154pp; English. XX CC The present invention describes a human tumour necrosis factor receptor CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive, dermatological, antiinflammatory, neuroprotective, antidiabetic, CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive CC CC activities, and can be used in gene therapy. (I) can be used for CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12 CC(e.g. ZTNF4), for treating disorders and diseases associated with B CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for CC inhibiting the proliferation of tumour cells. (I) is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia CC CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure CCor renal disease such as glomerulonephritis, vasculitis, chronic lymphoid CC leukaemia, nephritis, and pyelonephritis, and for treating renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or CCCCamyloidosis, hypertension, large vessel diseases, graft-versus host CC disease, graft rejection and Crohn's disease. (I) is useful for CC modulating the immune system, for regulating B cell responses and

development, for modulating development of other cells, antibody

in the exemplification of the present invention

production and cytokine production, and for modulating T and B cell

communication. The present sequence represents a protein which is given

CC

CC

CC

CC

```
XX
SQ
    Sequence 184 AA;
  Query Match
                       100.0%; Score 964; DB 5; Length 184;
                       100.0%; Pred. No. 7.6e-95;
  Best Local Similarity
 Matches 184; Conservative 0; Mismatches
                                             0;
                                                Indels
                                                          0;
                                                                     0;
                                                             Gaps
          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Qу
            Db
          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
            61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
            121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db
         181 ISAR 184
Qу
            \Box
         181 ISAR 184
Db
RESULT 8
ABP54694
    ABP54694 standard; protein; 184 AA.
ID
XX
AC
    ABP54694;
XX
DT
    30-DEC-2002 (first entry)
XX
DE
    Metastatic colorectal cancer-associated polypeptide.
XX
KW
    Colorectal cancer; metastasis; differential expression; cytostatic;
    diagnosis; gene therapy; vaccine.
KW
XX
OS
    Homo sapiens.
XX
    W0200268677-A2.
PN
XX
    06-SEP-2002.
PD
XX
PF
    27-FEB-2002; 2002WO-US006001.
XX
PR
    27-FEB-2001; 2001US-0272206P.
    02-APR-2001; 2001US-0281149P.
PR
    17-APR-2001; 2001US-0284555P.
PR
XX
PΑ
    (EOSB-) EOS BIOTECHNOLOGY INC.
    (UYCA-) UNIV CASE WESTERN RESERVE.
PΑ
XX
PΙ
    Mack DH, Markowitz SD;
XX
DR
    WPI; 2002-698677/75.
DR
    N-PSDB; ABQ81560.
```

XX

```
New genes that are up- or down-regulated in colorectal cancer, useful for
PT
PT
    diagnosing colorectal cancer in a subject, or for identifying modulators
PT
    of colorectal cancer-associated proteins and genes for treating
PT
    colorectal cancer.
XX
    Claim 8; Page 255; 260pp; English.
PS
XX
    The present sequence is the protein sequence of a human polypeptide
CC
    encoded by a gene that exhibits decreased expression in colon cancer-
CC
    derived metastases compared to normal colon tissue. It is an example of
CC
CC
    claimed polypeptides that are encoded by genes which are differentially
CC
    expressed in metastatic colorectal cancer cells. Such polypeptides are
CC
    useful in diagnostic and prognostic assays, for raising antibodies useful
CC
    e.g. in immunotherapy, and in screening for modulator compounds of
CC
    therapeutic value
XX
    Sequence 184 AA;
SQ
                        100.0%; Score 964; DB 5;
                                                  Length 184;
 Query Match
                        100.0%; Pred. No. 7.6e-95;
 Best Local Similarity
                                               0;
 Matches 184; Conservative
                            0; Mismatches
                                                   Indels
                                                            0;
                                                                Gaps
                                                                       0;
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Qy
             1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCL 60
Db
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
             61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
             121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db
         181 ISAR 184
Qу
             IIIII
         181 ISAR 184
Db
RESULT 9
AAE28961
    AAE28961 standard; protein; 184 AA.
ID
XX
AC
    AAE28961;
XX
    27-JAN-2003 (first entry)
DT
XX
DE
    Human B-cell maturation antigen (BCMA).
XX
KW
    Human; tumour; B-cell maturation antigen; transmembrane activator;
    calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;
KW
ΚŴ
    neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;
    non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
KW
KW
    BCMA; multiple myeloma.
XX
OS
    Homo sapiens.
XX
```

```
FΗ
    Key
                   Location/Qualifiers
FT
    Region
                   1. .54
FT
                   /note= "Antigenic epitope"
FT
                    1. .48
    Domain
FT
                    /note= "Extracellular domain"
FT
    Region
                    8. .41
FT
                    /note= "Cysteine rich region"
XX
    W0200266516-A2.
PN
XX
    29-AUG-2002.
PD
XX
ΡF
    06-FEB-2002; 2002WO-US003500.
XX
PR
    20-FEB-2001; 2001US-0270274P.
PR
    12-APR-2001; 2001US-0283447P.
XX
    (ZYMO ) ZYMOGENETICS INC.
PΑ
XX
PΤ
    Kindsvogel W;
XX
DR
    WPI; 2002-723183/78.
    N-PSDB; AAD46410.
DR
XX
PT
    B-cell maturation antigen and transmembrane activator and calcium-
PT
    modulator and cyclophilin ligand-interactor, useful for treating
PΤ
    disorders e.g. inflammation or lymphoma.
XX
PS
    Disclosure; Page 63; 67pp; English.
XX
CC
    The invention relates to the manufacture of a composition for inhibiting
CC
    the proliferation of tumour cells. The method involves using an antibody
    component that binds both the B-cell maturation antigen (BCMA) and the
CC
    transmembrane activator and calcium-modulator and cyclophilin liqand-
CC
CC
    interactor (TACI). BCMA and TACI binding antibody compositions are useful
CC
    for inhibiting proliferation of tumour cells, particularly inhibiting
CC
    ZTNF4 activity in a mammal associated with increased endogenous antibody
CC
    production or a disorder consisting of neoplasm, chronic lymphocytic
    leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
CC
    lymphoproliferative disease or light chain gammopathy or inflammation
CC
CC
    e.g. asthma. The invention is also useful in gene therapy. The present is
CC
    human BCMA protein
XX
SQ
    Sequence 184 AA;
                        100.0%; Score 964; DB 5; Length 184;
  Query Match
                        100.0%; Pred. No. 7.6e-95;
  Best Local Similarity
 Matches 184; Conservative 0; Mismatches
                                                                         0;
                                                0;
                                                   Indels
QУ
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
             Dh
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
QУ
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
             Db
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
```

```
Qу
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
              121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db
         181 ISAR 184
Qу
              1111
         181 ISAR 184
Db
RESULT 10
AAE35216
     AAE35216 standard; protein; 184 AA.
ID
XX
AC
    AAE35216;
XX
DT
    28-MAY-2003 (first entry)
XX
DE
    Human B-cell maturation receptor (BCMA) protein.
XX
KW
    Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
    TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
KW
KW
     anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
     glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
KW
    dermatological; neuroprotective; cyclophilin ligand-interactor; human;
KW
     autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
KW
KW
     diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
KW
     B-cell maturation receptor; BCMA; receptor.
XX
OS
    Homo sapiens.
XX
PN
    WO200294852-A2.
XX
    28-NOV-2002.
PD
XX
ΡF
    20-MAY-2002; 2002WO-US015910.
XX
PR
     24-MAY-2001; 2001US-0293343P.
XX
     (ZYMO ) ZYMOGENETICS INC.
PΑ
XX
    Rixon MW, Gross JA;
PI
XX
    WPI; 2003-148455/14.
DR
DR
    N-PSDB; AAD53754.
XX
PT
     Transmembrane activator and calcium modulator and cyclophilin ligand-
     interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
PT
РΤ
     diabetes, comprises a TACI receptor group and an immunoglobulin group.
XX
PS
     Disclosure; Col 100; 71pp; English.
XX
CC
     The invention relates to fusion proteins comprising transmembrane
     activator and calcium modulator and cyclophilin ligand-interactor (TACI)
CC
CC
     receptor group that binds tumour necrosis factor-like protein (ZTNF)2 or
     ZTNF4; and an immunoglobulin group comprising a constant region of an
CC
     immunoqlobulin. The invention is used to manufacture a medicament for
CC
CC
     inhibiting the proliferation of tumour cells in a mammalian subject. The
```

```
CC
    composition comprising the fusion protein may also be used in treating
CC
    autoimmune diseases (e.g. systemic lupus erythematosus, multiple
CC
    sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal
    diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft
CC
    rejection, anaemia and septic shock. The fusion proteins are also used in
CC
    gene therapy. The present sequence is human B-cell maturation receptor
CC
    (BCMA) protein used in the invention
CC
XX
SO
    Sequence 184 AA;
                        100.0%; Score 964; DB 6; Length 184;
 Query Match
                        100.0%; Pred. No. 7.6e-95;
 Best Local Similarity
                                                          0; Gaps
 Matches 184; Conservative 0; Mismatches
                                              0;
                                                  Indels
                                                                       0;
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Qу
             1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Db
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
QУ
             61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
             121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db
         181 ISAR 184
QУ
             | | | | |
Db
         181 ISAR 184
RESULT 11
ADA49361
TD
    ADA49361 standard; protein; 184 AA.
XX
AC
    ADA49361;
XX
DT
    20-NOV-2003 (first entry)
XX
DE
    Human BCMA protein.
XX
KW
    human; TALL-1; antagonist; immunosuppressive; antirheumatic;
    antiinflammatory; antiarthritic; dermatological; antidiabetic;
KW
    neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic;
KW
KW
    vaccine; autoimmune disease; rheumatoid arthriti;
    systemic lupus erythematosus; insulin dependent diabetes mellitus;
KW
KW
    multiple sclerosis; myasthaenia gravis; Grave's disease;
    autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;
KW
    Goodpasture's syndrome; pemphiqus vulgaris; acute rheumatic fever;
KW
KW
    post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.
XX
OS
    Homo sapiens.
XX
ΡN
    W02003035846-A2.
XX
PD
    01-MAY-2003.
XX
```

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PF
    24-OCT-2002; 2002WO-US034376.
XX
PR
    24-OCT-2001; 2001US-0345106P.
PR
    14-JAN-2002; 2002US-0348962P.
PR
    07-FEB-2002; 2002US-0354966P.
PR
    13-AUG-2002; 2002US-0403364P.
XX
PΑ
     (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
PΙ
    Zhang G, Shu H, Liu Y, Xu L;
XX
    WPI; 2003-403345/38.
DR
    N-PSDB; ADA49360.
DR
XX
    Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological
PΤ
    activity in mammal, has a modification in the region connecting beta
PT
    strands D and E that reduces the biological activity of TALL-1
PT
PT
    antagonist.
XX
    Claim 62; Page 613; 618pp; English.
PS
XX
    The invention relates to a novel TALL-1 antagonist protein, comprising a
CC
    sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEO ID
CC
    NO: 2, by at least one modification in the region connecting &bgr; strands
CC
    D and E that reduces the biological activity of the TALL- 1 antagonist as
CC
CC
    compared to wild-type TALL-1. A protein of the invention has
    immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
CC
    dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,
CC
    nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
CC
    a vaccine. A protein of the invention is useful for inhibiting TALL-1
CC
    biological activity in a mammal. TC is useful for treating autoimmune
CC
    diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
CC
    dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis,
CC
CC
    Grave's disease, autoimmune hemolytic anaemia, autoimmune
CC
    thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
    acute rheumatic fever, post-streptococcal glomerulonephritis and
CC
CC
    polyarteritis nodosa. The present sequence represents human BCMA.
XX
SQ
    Sequence 184 AA;
                        100.0%; Score 964; DB 6; Length 184;
 Query Match
                        100.0%; Pred. No. 7.6e-95;
 Best Local Similarity
 Matches 184; Conservative 0; Mismatches
                                                            0; Gaps
                                                                        0;
                                              0; Indels
           1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCL 60
Qy
             1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Db
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
             61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
QУ
             121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db
         181 ISAR 184
QУ
```

RESULT 12 ABP60552 ABP60552 standard; protein; 184 AA. ID XX AC ABP60552; XX DT28-MAR-2003 (first entry) XX DEHuman tumour necrosis factor BCMA. XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta; KW dermatological; immunosuppressive; antiinflammatory; antirheumatic; KW antiarthritic; cytostatic; antianaemic; antiallergic; antiasthmatic; KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic; KW KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD; KW inflammatory disorder; proliferative disorder; single chain antibody; KW antibody; human; BCMA; tumour necrosis factor. KW XX OS Homo sapiens. XX WO200294192-A2. ΡN XX 28-NOV-2002. PD XX PF22-MAY-2002; 2002WO-US016106. XX PR 24-MAY-2001; 2001US-0293100P. XX (HUMA-) HUMAN GENOME SCI INC. PΑ XX Ruben SM; PIXX WPI; 2003-156740/15. DR XX Novel isolated antibody that immunospecifically binds tumor necrosis PTfactor delta, useful for treating, preventing or ameliorating Non-PΤ Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's PTPTsyndrome. XX Disclosure; Page 222; 225pp; English. PS XX CC The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL). CC CC The antibody of the invention has dermatological, immunosuppressive, antiinflammatory, antirheumic, antiarthritic, cytostatic, antianaemic, CC CC antiallergic, antiasthmatic, neuroprotective, ophthalmological, CC tuberculostatic, antidiabetic, antipsoriatic, anti-HIV, antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity. CC The antibody or its fragment are useful for treating, preventing or CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in CC human, disease or disorder such as autoimmune disease, and graft versus CC CC host disease (GVHD). The autoimmune disease is systemic lupus

```
CC
    erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
CC
    is useful for detecting, diagnosing, prognosing, treating, preventing or
CC
    ameliorating a disease or disorder associated with aberrant APRIL or
    APRIL receptor expression or aberrant function of APRIL or APRIL
CC
    receptor. The disease or disorders includes autoimmune and inflammatory
CC
    disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
CC
    asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
CC
    uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
CC
    system, particularly B cell cancers, immune disorders such as myasthenia
CC
    gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
CC
    infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
CC
    proliferative disorders (e.g. leukemia). The present sequence represents
CC
    the tumour necrosis factor BCMA
CC
XX
SO
    Sequence 184 AA;
                        100.0%; Score 964; DB 6;
                                                  Length 184;
 Query Match
                                Pred. No. 7.6e-95;
 Best Local Similarity
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             1 MLOMAGOCSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
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Qу
             1111
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Db
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ID
XX
    ABP97717;
AC
XX
DT
    28-MAY-2003 (first entry)
XX
    Amino acid sequence of human BCMA receptor.
DE
XX
    Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KW
    TALL-1; April; systemic lupus erythematosus; BCMA.
KW
XX
OS
    Homo sapiens.
XX
ΡN
    WO2003014294-A2.
XX
PD
    20-FEB-2003.
XX
    24-JUL-2002; 2002WO-US023487.
PF
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XX
PR
    03-AUG-2001; 2001US-0310114P.
PR
    30-APR-2002; 2002US-0377171P.
XX
    (GETH ) GENENTECH INC.
PA
XX
    Dixit V, Grewal I, Ridgway J,
                                  Yan M;
PΙ
XX
    WPI: 2003-256560/25.
DR
    N-PSDB; ABZ68871.
DR
XX
    New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
PΤ
    preparing a composition for treating systemic lupus erythematosus.
PT
XX
    Disclosure; Fig 2; 153pp; English.
PS
XX
CC
    The present sequence represents a human BCMA polypeptide. The
    specification also describes TACI and BR3 polypeptides. TACI and BR3 are
CC
    receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
CC
    bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
CC
    BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
CC
    preparing a composition for treating systemic lupus erythematosus
CC
XX
    Sequence 184 AA;
SQ
                       100.0%; Score 964; DB 6; Length 184;
 Query Match
                      100.0%; Pred. No. 7.6e-95;
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 Matches 184; Conservative 0; Mismatches
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QУ
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Db
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Db
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ΤD
XX
AC
    ADD67527;
XX
DT
    15-JAN-2004 (first entry)
XX
DE
    Human Ly1732P protein SEQ ID NO:4.
XX
KW
    haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
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vaccine; immunotherapy; cancer; multiple myeloma cell;
KW
     chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
KW
KW
     human.
XX
OS
    Homo sapiens.
XX
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PN
XX
PD
     31-JUL-2003.
XX
     22-JAN-2003; 2003WO-US002353.
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XX
     22-JAN-2002; 2002US-00057475.
PR
XX
     (CORI-) CORIXA CORP.
PΑ
XX
     Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
PI
PΙ
     Carter L, Mcneill PD;
XX
    WPI; 2003-598749/56.
DR
     N-PSDB; ADD67526.
DR
XX
     New hematological malignancy-related genes and polypeptides, useful for
PT
     screening anti-cancer agents, and generating antibodies or
PT
     immunoconjugates for treating e.g. multiple myeloma cell or chronic
PT
PT
     lymphocytic leukemia.
XX
     Claim 9; SEQ ID NO 4; 307pp; English.
PS
XX
     The present invention describes an isolated polynucleotide (I), which is
CC
     overexpressed in haematological malignancies, and which encodes a
CC
     polypeptide or an immunogenic fragment of the polypeptide. Also
CC
     described: (1) an isolated polypeptide; (2) an expression vector
CC
     comprising (I) operably linked to an expression control sequence; (3) a
CC
     host cell comprising an expression vector; (4) an isolated antibody that
CC
     specifically binds to the polypeptide or its immunogenic fragment; and
CC
     (5) immunoconjugates comprising the antibody above, or an antibody that
CC
     specifically binds to a polypeptide, or its immunogenic fragment, encoded
CC
     by (I). (I) has cytostatic and immunostimulant activities, and can be
CC
     used in vaccines and immunotherapy. The immunoconjugates are useful in
CC
     the manufacture of a medicament, particularly as active ingredients in a
CC
     composition for treating cancer, e.g. multiple myeloma cell, chronic
CC
     lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,
СC
     primates, goats, bovines, equines, porcines, lupines, canines or felines.
CC
     The polynucleotide (I) or polypeptide can be used for screening anti-
CC
     cancer agents, and generating antibodies or immunoconjugates for treating
CC
     or preventing the above-mentioned diseases. The polynucleotide,
CC
     polypeptide or antibody can be used for detecting, diagnosing or
CC
     prognosticating the haematological malignancies described above. The
CC
     present sequence is used in the exemplification of the present invention.
CC
XX
SO
     Sequence 184 AA;
                          100.0%; Score 964; DB 7; Length 184;
  Query Match
                          100.0%; Pred. No. 7.6e-95;
  Best Local Similarity
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Db
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ΟV
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Db
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XX
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    27-JUN-2003 (first entry)
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    Human Genoxit.
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    Human; genoxit; anorectic; antilipaemic; antiarteriosclerotic; cardiant;
KW
    antidiabetic; hypotensive; ophthalmological; neuroprotective;
KW
    nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family;
KW
    Type III transmembrane protein; insulin resistance; atherosclerosis;
KW
    atheromatous disease; heart disease; hypertension; stroke; syndrome X;
KW
    diabetes mellitus; hyperlipidaemia; hyperuricaemia.
KW
XX
OS
    Homo sapiens.
XX
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    Domain
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PN
XX
PD
    20-FEB-2003.
XX
    05-AUG-2002; 2002WO-IB003498.
PF
XX
    06-AUG-2001; 2001US-0310754P.
PR
XX
    (GEST ) GENSET SA.
PΑ
XX
PΙ
    Lucas J, Dialynas D, Briggs K;
```

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XX
DR
    WPI; 2003-268160/26.
DR
    N-PSDB; ACC00340.
XX
    New use of agonist or antagonist of Genoxit activity for preventing or
PΤ
PΤ
    treating obesity-related diseases or disorders, e.g. hyperlipidemia and
PΤ
    atherosclerosis.
XX
    Disclosure; Page 32; 35pp; English.
PS
XX
    The present invention relates to the use of an agonist or antagonist of
CC
CC
    Genoxit activity for preventing or treating obesity. Genoxit is a member
    of the Tumour Necrosis Factor Receptor Super Family and is a Type III
CC
    transmembrane protein. The agonists or antagonists of the invention are
CC
CC
    useful for treating or preventing obesity-related diseases or disorders,
    e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
CC
    heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
CC
    blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
CC
    (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic
CC
CC
    complications, e.g. microangiopathic lesions, ocular lesions,
    retinopathy, neuropathy and renal lesions
CC
XX
    Sequence 184 AA;
SO
                               Score 958; DB 6; Length 184;
 Query Match
                       99.4%;
                              Pred. No. 3.3e-94;
 Best Local Similarity
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Db
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Db
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Db
         181 ISAR 184
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         181 ISAR 184
Db
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Search completed: April 19, 2004, 13:20:57 Job time: 40.2387 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:19:08; Search time 12.4938 Seconds

(without alignments)

760.310 Million cell updates/sec

Title: PCT-US03-05147-1

Perfect score: 964

Sequence: 1 MLQMAGQCSQNEYFDSLLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	 964	100.0	184	4	US-09-565-423-11	Sequence 11, Appl
2	572	59.3	185	4	US-09-565-423-17	Sequence 17, Appl
3	79.5	8.2	1009	2	US-08-357-642A-1	Sequence 1, Appli
4	79.5	8.2	1009	2	US-08-460-626-1	Sequence 1, Appli
5	78.5	8.1	293	2	US-08-810-572A-2	Sequence 2, Appli
б	78.5	8.1	293	4	US-09-290-333-2	Sequence 2, Appli
7	78.5	8.1	293	4	US-09-782-857A-2	Sequence 2, Appli
8	78.5	8.1	293	4	US-09-879-919 - 22	Sequence 22, Appl
9	78.5	8.1	293	4	US-09-848-295-4	Sequence 4, Appli
10	76	7.9	744	1	US-08-179-481-2	Sequence 2, Appli
11	75	7.8	857	1	US-07-717-331F-2	Sequence 2, Appli

12	71.5	7.4	835	4	US-09-489-039A-8740	Sequence	8740, Ap
13	71	7.4	333	4	US-09-328-352-6022	Sequence	6022, Ap
14	70.5	7.3	154	4	US-09-232-160-18	Sequence	18, Appl
15	69.5	7.2	166	2	US-08-810-572A-6	Sequence	6, Appli
16	69.5	7.2	166	4	US-09-290-333-6	Sequence	6, Appli
17	69,5	7.2	166	4	US-09-782-857A-6	Sequence	6, Appli
18	69.5	7.2	217	4	US-09-252-991A-30641	Sequence	30641, A
19	69.5	7.2	224	4	US-09-465-901-30	Sequence	30, Appl
20	69.5	7.2	353	4	US-09-328-352-5429	Sequence	5429, Ap
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33	69	7.2	324	2	US-08-579-940-7	Sequence	7, Appli
34	69	7.2	445	1	US-08-353-400-33	Sequence	33, Appl
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36	69	7.2	464	1	US-08-353-400-36	Sequence	36, Appl
37	69	7.2	599	1	US-08-442-542-18	Sequence	18, Appl
38	69	7.2	599	3	US-08-765-469-18	Sequence	18, Appl
39	68.5	7.1	228	4	US-09-107-532A-3896	Sequence	3896, Ap
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42	68.5	7.1	877	1	US-08-072-574-12	Sequence	12, Appl
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44	68.5	7.1	877	3	US-08-367-264-12	Sequence	12, Appl
45	68.5	7.1	877	4	US-09-153-757-12	Sequence	12, Appl

ALIGNMENTS

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RESULT 1
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; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
 TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 11

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 Query Match
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; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
  APPLICANT: Shu, Hong-Bing
  TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
  TITLE OF INVENTION: METHODS OF USE THEREOF
  FILE REFERENCE: 2879-72
  CURRENT APPLICATION NUMBER: US/09/565,423
  CURRENT FILING DATE: 2000-05-05
  PRIOR APPLICATION NUMBER: UNKNOWN
  PRIOR FILING DATE: 2000-05-01
  PRIOR APPLICATION NUMBER: 60/132,892
  PRIOR FILING DATE: 1999-05-06
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RESULT 3
US-08-357-642A-1
; Sequence 1, Application US/08357642A
; Patent No. 5837524
  GENERAL INFORMATION:
    APPLICANT: Sima Lev
    APPLICANT: Joseph Schlessinger
    TITLE OF INVENTION: PYK2 RELATED PRODUCTS
   TITLE OF INVENTION: AND METHODS
   NUMBER OF SEQUENCES: 16
   CORRESPONDENCE ADDRESS:
    ADDRESSEE: Lyon & Lyon
     STREET: 633 West Fifth Street
STREET: Suite 4700
;
     CITY: Los Angeles
     STATE: California
     COUNTRY: U.S.A.
     ZIP: 90071-2066
   COMPUTER READABLE FORM:
     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
      MEDIUM TYPE: storage
     COMPUTER: IBM Compatible
     OPERATING SYSTEM: IBM P.C. DOS 5.0
     SOFTWARE: Word Perfect 5.1
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    APPLICATION NUMBER: US/08/357,642A
      FILING DATE: December 15, 1994
     CLASSIFICATION: 536
   PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
     FILING DATE:
   ATTORNEY/AGENT INFORMATION:
     NAME: Warburg, Richard J.
;
      REGISTRATION NUMBER: 32,327
;
      REFERENCE/DOCKET NUMBER: 209/070
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: (213) 489-1600
      TELEFAX: (213) 955-0440
      TELEX: 67-3510
  INFORMATION FOR SEQ ID NO: 1:
   SEQUENCE CHARACTERISTICS:
     LENGTH: 1009
     TYPE: amino acid
     STRANDEDNESS: single
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TOPOLOGY: linear
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RESULT 4
US-08-460-626-1
; Sequence 1, Application US/08460626
; Patent No. 5837815
; GENERAL INFORMATION:
   APPLICANT: SIMA LEV
    APPLICANT: JOSEPH SCHLESSINGER
  TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND TITLE OF INVENTION: METHODS
  NUMBER OF SEQUENCES: 25
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Lyon & Lyon
     STREET: 633 West Fifth Street
     STREET: Suite 4700
;
     CITY: Los Angeles
     STATE: California
;
     COUNTRY: U.S.A.
     ZIP: 90071-2066
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    MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
     MEDIUM TYPE: storage
     COMPUTER: IBM Compatible
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;
     SOFTWARE: Word Perfect 5.1
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     FILING DATE: June 2, 1995
     CLASSIFICATION: 435
;
   PRIOR APPLICATION DATA:
;
     APPLICATION NUMBER: 08/357,642
;
      FILING DATE: December 15, 1994
    ATTORNEY/AGENT INFORMATION:
     NAME: Warburg, Richard J.
      REGISTRATION NUMBER: 32,327
      REFERENCE/DOCKET NUMBER: 211/121
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (213) 489~1600
      TELEFAX: (213) 955-0440
      TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
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```
SEQUENCE CHARACTERISTICS:
      LENGTH: 1009
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;
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: peptide
US-08-460-626-1
                        8.2%; Score 79.5; DB 2; Length 1009;
 Query Match
 Best Local Similarity 32.1%; Pred. No. 3.8;
         25; Conservative 9; Mismatches 29; Indels
                                                         15; Gaps
          88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
Qу
            249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
Db
         139 DSDHCFPLPAMEEGATIL 156
Qy
            306 RSIRCLPL---EEGQAVL 320
Dh
RESULT 5
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
   APPLICANT: Bram, Richard J.
    APPLICANT: von Bulow, Gotz
    TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
    TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
USE
    TITLE OF INVENTION: THEREOF
;
   NUMBER OF SEQUENCES: 11
;
   CORRESPONDENCE ADDRESS:
     ADDRESSEE: David A. Jackson, Esq.
     STREET: 411 Hackensack Ave, Continental Plaza, 4th
     STREET: Floor
     CITY: Hackensack
     STATE: New Jersey
     COUNTRY: USA
;
     ZIP: 07601
   COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
;
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
;
      SOFTWARE: PatentIn Release #1.0, Version #1.30
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/810,572A
      FILING DATE: 28-FEB-1997
      CLASSIFICATION: 536
    ATTORNEY/AGENT INFORMATION:
      NAME: Jackson Esq., David A.
      REGISTRATION NUMBER: 26,742
     REFERENCE/DOCKET NUMBER: 1340-1-007
    TELECOMMUNICATION INFORMATION:
    TELEPHONE: 201-487-5800
      TELEFAX: 201-343-1684
```

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INFORMATION FOR SEQ ID NO: 2:
   SEQUENCE CHARACTERISTICS:
    LENGTH: 293 amino acids
;
     TYPE: amino acid
;
     STRANDEDNESS: single
     TOPOLOGY: linear
  MOLECULE TYPE: protein
  HYPOTHETICAL: NO
   FRAGMENT TYPE: N-terminal
    ORIGINAL SOURCE:
     ORGANISM: Homo sapiens
US-08-810-572A-2
 Query Match
                     8.1%; Score 78.5; DB 2; Length 293;
 Best Local Similarity 19.9%; Pred. No. 0.86;
 Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;
         8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
Qу
           34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
Db
         66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS--- 107
Qγ
                 93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
Db
        108 ---RTGDEIILPRG-----KVD 139
QУ
              : |:: |
                                        |: :|:|: |:|
        152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
Db
       140 SDHCFPLPAMEEGATILVTTKTNDYC 165
Qу
           Db
        210 QDH----AMEAGSPVSTSPEPVETC 230
RESULT 6
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
 GENERAL INFORMATION:
      APPLICANT: Bram, Richard J.
                von Bulow, Gotz
      TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
                        CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS
OF USE
;
       NUMBER OF SEQUENCES: 11
       CORRESPONDENCE ADDRESS:
           ADDRESSEE: David A. Jackson, Esq.
           STREET: 411 Hackensack Ave, Continental Plaza, 4th
                  Floor
           CITY: Hackensack
           STATE: New Jersey
           COUNTRY: USA
           ZIP: 07601
       COMPUTER READABLE FORM:
           MEDIUM TYPE: Floppy disk
           COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
;
            SOFTWARE: PatentIn Release #1.0, Version #1.30
        CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/290,333
            FILING DATE: 12-Apr-1999
            CLASSIFICATION: <Unknown>
        ATTORNEY/AGENT INFORMATION:
            NAME: Jackson Esq., David A.
            REGISTRATION NUMBER: 26,742
            REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
        TELECOMMUNICATION INFORMATION:
            TELEPHONE: 201-487-5800
            TELEFAX: 201-343-1684
  INFORMATION FOR SEQ ID NO: 2:
        SEQUENCE CHARACTERISTICS:
            LENGTH: 293 amino acids
            TYPE: amino acid
            STRANDEDNESS: single
            TOPOLOGY: linear
       MOLECULE TYPE: protein
       HYPOTHETICAL: NO
       FRAGMENT TYPE: N-terminal
      ORIGINAL SOURCE:
            ORGANISM: Homo sapiens
       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2
 Query Match
                      8.1%; Score 78.5; DB 4; Length 293;
 Best Local Similarity 19.9%; Pred. No. 0.86;
 Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;
Qу
          8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
           34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
Db
         66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
Qу
                 Db
         93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
        108 ---RTGDEIILPRG------KVD 139
Qу
                                                           1
               : |:: |
                                          1: : |:|: :|:|
Db
        152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
        140 SDHCFPLPAMEEGATILVTTKTNDYC 165
QУ
                 210 QDH----AMEAGSPVSTSPEPVETC 230
Db
RESULT 7
US-09-782-857A-2
; Sequence 2, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
       APPLICANT: Bram, Richard J.
                 von Bulow, Gotz
   TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
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CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS
OF USE
                           THEREOF
        NUMBER OF SEQUENCES: 10
        CORRESPONDENCE ADDRESS:
             ADDRESSEE: David A. Jackson, Esq.
             STREET: 411 Hackensack Ave, Continental Plaza, 4th
                    Floor
             CITY: Hackensack
             STATE: New Jersey
             COUNTRY: USA
             ZIP: 07601
        COMPUTER READABLE FORM:
            MEDIUM TYPE: Floppy disk
             COMPUTER: IBM PC compatible
             OPERATING SYSTEM: PC-DOS/MS-DOS
             SOFTWARE: PatentIn Release #1.0, Version #1.30
       CURRENT APPLICATION DATA:
            APPLICATION NUMBER: US/09/782,857A
             FILING DATE: 14-Feb-2001
            CLASSIFICATION: <Unknown>
        PRIOR APPLICATION DATA:
            APPLICATION NUMBER: 08/810,572
             FILING DATE: <Unknown>
        ATTORNEY/AGENT INFORMATION:
            NAME: Jackson Esq., David A.
             REGISTRATION NUMBER: 26,742
            REFERENCE/DOCKET NUMBER: 1340-1-007
        TELECOMMUNICATION INFORMATION:
            TELEPHONE: 201-487-5800
            TELEFAX: 201-343-1684
  INFORMATION FOR SEQ ID NO: 2:
       SEQUENCE CHARACTERISTICS:
            LENGTH: 293 amino acids
            TYPE: amino acid
            STRANDEDNESS: single
            TOPOLOGY: linear
      MOLECULE TYPE: protein
       HYPOTHETICAL: NO
       FRAGMENT TYPE: N-terminal
        ORIGINAL SOURCE:
             ORGANISM: Homo sapiens
        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2
 Query Match
                        8.1%; Score 78.5; DB 4; Length 293;
 Best Local Similarity 19.9%; Pred. No. 0.86;
 Matches 41; Conservative 35; Mismatches
                                              73; Indels 57; Gaps
QУ
          8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
            Db
          34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
Qу
          66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS--- 107
                    Db
          93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
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108 ---RTGDEIILPRG-----KVD 139
Qу
                                        1: : |:|: :|:|
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Db
        152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
       140 SDHCFPLPAMEEGATILVTTKTNDYC 165
Qу
            Db
        210 QDH----AMEAGSPVSTSPEPVETC 230
RESULT 8
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
  PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
 PRIOR FILING DATE: 2000-12-13
  PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
  LENGTH: 293
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-879-919-22
 Query Match
                     8.1%; Score 78.5; DB 4; Length 293;
 Best Local Similarity 19.9%; Pred. No. 0.86;
 Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;
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         8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
          34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
Db
         66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS--- 107
QУ
                 Db
        93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
Qy
        108 ---RTGDEIILPRG-----KVD 139
               : |:: |
                                       |: : |:|: :|:|
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Db
         152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
        140 SDHCFPLPAMEEGATILVTTKTNDYC 165
QУ
                  11
Db
         210 QDH----AMEAGSPVSTSPEPVETC 230
RESULT 9
US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
  APPLICANT: Ruben, Steven M.
  TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
  TITLE OF INVENTION: Thereon
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
  LENGTH: 293
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-848-295-4
 Query Match
                      8.1%; Score 78.5; DB 4; Length 293;
 Best Local Similarity 19.9%; Pred. No. 0.86;
 Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps
Qу
          8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
           34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
Db
         66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
Qу
                  11 1 1: 1:: 1:
Db
         93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
        108 ---RTGDEIILPRG-----KVD 139
QУ
                                         |: :|:|: :|:|
Db
        152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
QУ
        140 SDHCFPLPAMEEGATILVTTKTNDYC 165
                 11
Db
        210 QDH----AMEAGSPVSTSPEPVETC 230
RESULT 10
US-08-179-481-2
; Sequence 2, Application US/08179481
; Patent No. 5624816
; GENERAL INFORMATION:
   APPLICANT: CARRAWAY, KERMIT L.
   APPLICANT: CAROTHERS CARRAWAY, CORALIE A.
```

```
APPLICANT: FREGIEN, NEVIS L.
   TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
  NUMBER OF SEQUENCES: 125
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
     STREET: 1100 NEW YORK AVENUE, N.W.
     CITY: WASHINGTON
    STATE: D.C.
    COUNTRY: U.S.A.
     ZIP: 20005-3918
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
     COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/179,481
    FILING DATE: 28-DEC-1993
     CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/922,521
     FILING DATE: 30-JUL-1992
  ATTORNEY/AGENT INFORMATION:
    NAME: KOKULIS, PAUL N.
    REGISTRATION NUMBER: 16,773
    REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
    TELECOMMUNICATION INFORMATION:
     TELEPHONE: (202) 861-3000
     TELEFAX: (202) 822-0944
    TELEX: 6714627 CUSH
  INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 744 amino acids
     TYPE: amino acid
     TOPOLOGY: linear
   MOLECULE TYPE: protein
US-08-179-481-2
 Query Match
                      7.9%; Score 76; DB 1; Length 744;
 Best Local Similarity 22.1%; Pred. No. 6.3;
 Matches 34; Conservative 29; Mismatches 57; Indels 34; Gaps 6;
         4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC-----NASVTNSVKGT 52
Qу
           Db
         49 LEGRTAQTDSANATNFIAFAAQYNTSSLKSPITVQWFLEPNDTIRVVHNNOTVAFNTSDT 108
        53 NAI-LWTCLGLSLI------ISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLG 98
QУ
            ::: |: |: |: |: |::: | |: |::: | || ||
Db
        109 EDLPVFNATGVLLIQNGSQVSANFDGTVTISVIALSNILHASSS--LSEEYRNHTKGLLG 166
        99 MANIDLEKSRTGDEIILPRGLEYTVEECTCEDCI 132
Qу
           167 VWNDNPE----DDFRMPNG--STIPSNTSEETL 193
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RESULT 11 US-07-717-331F-2

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; Sequence 2, Application US/07717331F
; Patent No. 5484905
  GENERAL INFORMATION:
    APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
    APPLICANT: Stein
    TITLE OF INVENTION: A Receptor Protein Kinase Gene
    TITLE OF INVENTION: Encoded At The Self-Incompatability Locus
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
     ADDRESSEE: Yahwak & Associates
     STREET: 25 Skytop Drive
     CITY: Trumbull
     STATE: Connecticut
     COUNTRY: USA
     ZIP: 06611
   COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy Disk
     COMPUTER: Macintosh
    OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
;
   CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/07/717,331F
      FILING DATE: June 19th 1991
     CLASSIFICATION: 800
   ATTORNEY/AGENT INFORMATION:
    NAME: George M. Yahwak
     REGISTRATION NUMBER: 26,824
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (203)268-1951
      TELEFAX: (203)268-1951
  INFORMATION FOR SEQ ID NO: 2:
   SEQUENCE CHARACTERISTICS:
     LENGTH: 857 amino acids
     TYPE: amino acid
     TOPOLOGY: linear
   MOLECULE TYPE: peptide
US-07-717-331F-2
 Query Match
                       7.8%; Score 75; DB 1; Length 857;
 Best Local Similarity 17.6%; Pred. No. 10;
 Matches 33; Conservative 30; Mismatches 50; Indels 74; Gaps 7;
          24 CQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWT------ 58
Qу
            1: || |: || : || : ||
Db
         380 CKKRCISD---CNCTAFANADIRNG--GSGCVIWTERLEDIRNYATDAIDGQDLYVRLAA 434
         59 -----CLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
QУ
                       435 ADIAKKRNASGKIISLTVGVSVLLLLIMFCL-----WKRKQKRAKASAISIANTQRNQ 487
Db
        107 SRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCF----PLPAMEEGATILVTTKT 161
QУ
                                   488 NLPMNEMVL------SSKREFSGEYKFEELELPLIEME---TVVKATEN 527
Db
Qу
        162 NDYCKSL 168
              1 1
Db 528 FSSCNKL 534
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RESULT 12
US-09-489-039A-8740
; Sequence 8740, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
  FILE REFERENCE: 2709.2004001
  CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8740
  LENGTH: 835
   TYPE: PRT
   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8740
  Query Match
                       7.4%; Score 71.5; DB 4; Length 835;
  Best Local Similarity 21.0%; Pred. No. 25;
 Matches 56; Conservative 36; Mismatches 80; Indels 95; Gaps 14;
          1 MLQMAGQCSQNE------YFDSLLHACIP---CQL------RCSSNTPPLT 36
Qу
            Db
         199 MILMAGFTAGNEKGELVVLGRNGSDYSAAVLAACLRADCCEIWTDVDGVYTCDPROVP-- 256
         37 CQRYCNASVTNSVKGTNAILWTCLGLSL----IISLAVFVLMFLLRKISSEPL---- 85
Qу
                :|: |: |: |: |: |::
         257 -----DARLLKSMSYQEAMELSYFGAKVLHPRTIAPIAQFQIPCLIKNTGNPQAPGTLIG 311
Db
         86 --KDE----FKNTGSGLLGM----ANIDLEKSRTGDEIIL--PRGLEY 121
Qу
                   | :| |: || |: || ||
         312 ASRDEDDLPVKGISNLNNMAMFNVSGPGMKGMVGMAARVFATMSRAGISVVLITQSSSEY 371
Db
        122 TVEECTCE-DCIKSKPKVDSDHCF-----PLPAMEEGATILVTTKTNDYCKSLP--- 169
QУ
            :: | : || ::| :: :
                                        372 SISFCVPQSDCARAKRAMEDEFYLELKEGLLEPLAIMERLAIISV---VGDGMRTLRGIS 428
Db
        170 ----AALSATEI-----EKSIS 182
QУ
               |||: |
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Db
         429 AKFFAALARANINIVAIAQGSSERSIS 455
RESULT 13
US-09-328-352-6022
; Sequence 6022, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
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; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6022
   LENGTH: 333
   TYPE: PRT
   ORGANISM: Acinetobacter baumannii
US-09-328-352-6022
 Query Match 7.4%; Score 71; DB 4; Length 333; Best Local Similarity 24.7%; Pred. No. 7.7;
 Matches 36; Conservative 29; Mismatches 67; Indels 14; Gaps
          45 VTNSVKGTNAI-LWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANI- 102
QУ
            Db
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         103 -DLEKSRTGDEIILPR------GLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGA 153
Qу
             Db
          65 RDIRLLNYGN-VVNPQLTDTTPWGGIVLTGSTATNANNINFIPKVDTNTYIPEALLSRGA 123
        154 TILVTTKTNDYCKSLPAALSATEIEK 179
Qу
               |:| |:: | | ::: |:
         124 GDTVST-VNNHWKGLSNIQNSSNAEE 148
RESULT 14
US-09-232-160-18
; Sequence 18, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
  APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
 TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
  CURRENT FILING DATE: 1999-01-15
  NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PERL Program
; SEQ ID NO 18
  LENGTH: 154
   TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE: ~
   OTHER INFORMATION: 1299627
US-09-232-160-18
                       7.3%; Score 70.5; DB 4; Length 154;
 Query Match
 Best Local Similarity 25.2%; Pred. No. 2.9;
 Matches 30; Conservative 16; Mismatches 52; Indels 21; Gaps 6;
Qy
         13 YFDSLLHAC-IPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLG----LSLIIS 67
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Dh
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          68 LAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEEC 126
Qy
             :|: : | :
                          : | |:| :|: |
                                                        | | | :: :| |
Db
          80 IAICICMCM-----KNHRATRVGILRTTHINTVSSYPGPP---PYGHDHEMEYC 125
RESULT 15
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
  GENERAL INFORMATION:
    APPLICANT: Bram, Richard J.
    APPLICANT: von Bulow, Gotz
    TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
    TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
USE
    TITLE OF INVENTION: THEREOF
;
    NUMBER OF SEQUENCES: 11
;
    CORRESPONDENCE ADDRESS:
     ADDRESSEE: David A. Jackson, Esq.
     STREET: 411 Hackensack Ave, Continental Plaza, 4th
     STREET: Floor
     CITY: Hackensack
     STATE: New Jersey
     COUNTRY: USA ZIP: 07601
;
;
   COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
     COMPUTER: IBM PC compatible
     OPERATING SYSTEM: PC-DOS/MS-DOS
;
     SOFTWARE: PatentIn Release #1.0, Version #1.30
;
   CURRENT APPLICATION DATA:
;
     APPLICATION NUMBER: US/08/810,572A
     FILING DATE: 28-FEB-1997
;
      CLASSIFICATION: 536
   ATTORNEY/AGENT INFORMATION:
     NAME: Jackson Esq., David A.
     REGISTRATION NUMBER: 26,742
     REFERENCE/DOCKET NUMBER: 1340-1-007
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 201-487-5800
      TELEFAX: 201-343-1684
  INFORMATION FOR SEQ ID NO: 6:
   SEQUENCE CHARACTERISTICS:
     LENGTH: 166 amino acids
;
      TYPE: amino acid
      STRANDEDNESS: single
;
      TOPOLOGY: linear
   MOLECULE TYPE: peptide
   HYPOTHETICAL: NO
    FRAGMENT TYPE: N-terminal
    ORIGINAL SOURCE:
      ORGANISM: Homo sapiens
US-08-810-572A-6
```

Best Local Similarity 25.0%; Pred. No. 4.2;
Matches 15; Conservative 14; Mismatches 28; Indels 3; Gaps 2;

Qy 8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
| : : | : | | : : | : : | : : | : : |

Db 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92

Search completed: April 19, 2004, 13:24:20 Job time: 13.4938 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:18:32; Search time 10.2222 Seconds

(without alignments)

1731.447 Million cell updates/sec

Title: PCT-US03-05147-1

Perfect score: 964

Sequence: 1 MLQMAGQCSQNEYFDSLLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Se .				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	964	100.0	184	2	S43486	B-cell maturation
2	88.5	9.2	217	2	C97344	amino acid ABC tra
3	86.5	9.0	858	2	T08881	prominin - mouse
4	83.5	8.7	1998	2	T13009	hypothetical prote
5	82	8.5	1009	2	A57434	protein-tyrosine k
6	81.5	8.5	2233	2	T28669	surface protein 51
7	81	8.4	773	2	D89010	protein R08F11.7 [
8	79.5	8.2	1009	2	S60248	protein-tyrosine k
9	79.5	8.2	1299	2	T43251	furin (EC 3.4.21.7
10	78.5	8.1	343	2	D64469	potassium channel
11	78	8.1	841	2	JC5894	killer cell inhibi
12	77.5	8.0	738	2	D86345	hypothetical prote
13	77.5	8.0	968	2	T01733	hypothetical prote

14	77	8.0	522	2	T45824
15	77	8.0	539	2	F72288
16	76.5	7.9	357	2	T21152
17	76.5	7.9	1404	2	T19277
18	76	7.9	744	2	A43353
19	76	7.9	748	2	T47250
20	75.5	7.8	638	2	T41478
21	75	7.8	450	2	в97297
22	75	7.8	857	1	A41369
23	74.5	7.7	384	2	S45592
24	74.5	7.7	1101	2	T16840
25	74	7.7	377	2	JC7535
26	73.5	7.6	307	2	В95099
27	73.5	7.6	307	2	A97967
28	73	7.6	304	2	A89882
29	73	7.6	679	2	В96599
30	73	7.6	733	1	A46373
31	72.5	7.5	243	2	T31144
32	72.5	7.5	408	2	B84518
33	72	7.5	416	2	s75097
34	72	7.5	855	2	T10665
35	71.5	7.4	105	2	T10350
36	71.5	7.4	627	2	B71709
37	71	7.4	227	2	F72334
38	71	7.4	414	2	G71331
39	71	7.4	473	2	AF1207
40	71	7.4	480	2	G88690
41	71	7.4	500	2	T10543
42	71	7.4	660	2	T02768
43	70.5	7.3	188	2	н82933
44	70.5	7.3	412	2	T24023
45	70.5	7.3	424	2	T14525

hypothetical prote methyl-accepting c hypothetical prote hypothetical prote ascites sialoglyco complex I intermed probable transcrip hydrogenase chain S-receptor kinase ERD1 protein - yea hypothetical prote chitinase (EC 3.2. membrane protein [conserved hypothet hypothetical prote protein F20N2.12 [probable serine/th hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote conserved hypothet probable cell divi ABC transporters (protein F41H10.1 [hypothetical prote spike glycoprotein hypothetical prote hypothetical prote S-locus-specific q

ALIGNMENTS

RESULT 1 S43486 B-cell maturation factor - human N; Alternate names: BCM protein; BCMA protein; BEL protein C; Species: Homo sapiens (man) C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text change 21-Jul-2000 C; Accession: S43486; S31208; S36661 R; Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A. Nucleic Acids Res. 22, 1147-1154, 1994 A; Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidirectionally transcribed. A; Reference number: S43486; MUID: 94218235; PMID: 8165126 A; Accession: S43486 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-184 < LAA>

A;Cross-references: EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471245 R;Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.;

Tsapis, A. EMBO J. 11, 3897-3904, 1992

```
A; Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by
a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.
A; Reference number: S31208; MUID: 93010984; PMID: 1396583
A; Accession: S31208
A; Molecule type: mRNA
A; Residues: 1-184 <LA2>
A;Cross-references: EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PID:g29408
A; Accession: S36661
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 4-184 < LA3 >
A; Cross-references: EMBL: Z14955
C:Genetics:
A; Gene: GDB: BCMA
A; Cross-references: GDB:135977; OMIM:109545
A; Map position: 16p13.1-16p13.1
A; Introns: 44/1; 93/1
C; Superfamily: human B-cell maturation factor
  Query Match
                        100.0%; Score 964; DB 2; Length 184;
  Best Local Similarity
                        100.0%; Pred. No. 6.1e-81;
 Matches 184; Conservative 0; Mismatches
                                              0; Indels
                                                                        0;
Qу
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
             Db
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
QУ
             Db
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy
             Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
         181 ISAR 184
QУ
             \perp
Db
         181 ISAR 184
RESULT 2
C97344
amino acid ABC transporter, permease component CAC3619 [imported] - Clostridium
acetobutylicum
C; Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence revision 14-Sep-2001 #text change 30-Sep-2001
C; Accession: C97344
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson,
R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.;
Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.;
Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing
Bacterium Clostridium acetobutylicum.
A; Reference number: A96900; MUID: 21359325; PMID: 21359325
A; Accession: C97344
A; Status: preliminary
```

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A; Molecule type: DNA
A; Residues: 1-217 <KUR>
A; Cross-references: GB: AE001437; PIDN: AAK81542.1; PID: g15026719; GSPDB: GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
A; Gene: CAC3619
C; Superfamily: histidine permease protein M
  Query Match
                       9.2%; Score 88.5; DB 2; Length 217;
  Best Local Similarity 24.8%; Pred. No. 0.99;
         55; Conservative 25; Mismatches 77; Indels 65; Gaps 10;
  Matches
          16 SLLHACIPCQLRCSSNTPPLTCQRYCNASV-----TNSVKGTNAI----LWTCLGL 62
QУ
            Db
          4 SSLNKVIPVLLDGTRITLLLTCSSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT 63
          63 SLIISLAVFV--LMFLLRKISSEPLKDEF----KNTGS-----GLLGMANIDLEKSR 108
Qy
             Dh
         64 PLLLQLYVYYYGLPFLSDKLTMTPMKAAILGLSLNSGAYIAEIIRGGILAIDNGQFEASK 123
QУ
        109 -----TGDEIILPRGLEYTVEEC-----TCEDCI-KSKPKVDSDH 142
                   Db
        124 ALGLTYGQTMKRIILPQAIRVVIPPCGNEFIAMIKDTSLVSVITMEELLRKAQLLVSSSG 183
Qу
         143 CFPLPAMEEGA--TILVTTKTNDYCKSLPAALSATEIEKSIS 182
                1: | | | | | : |
Db
        184 DAVTPYLFAGIFYLILTTIFTGIFSK-----IEKKLS 215
RESULT 3
T08881
prominin - mouse
C; Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text change 21-Jul-2000
C; Accession: T08881
R; Weigmann, A.; Corbeil, D.; Hellwig, A.; Huttner, W.B.
Proc. Natl. Acad. Sci. U.S.A. 94, 12425-12430, 1997
A; Title: Prominin, a novel microvilli-specific polytopic membrane protein of the
apical surface of epithelial cells, is targeted to plasmalemmal protrusions of
non-epithelial cells.
A; Reference number: Z16512; MUID: 98024147; PMID: 9356465
A; Accession: T08881
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-858 <WEI>
A;Cross-references: EMBL:AF026269; NID:g2559003; PIDN:AAB86715.1; PID:g2559004
A; Experimental source: kidney
C; Keywords: glycoprotein; membrane protein
 Query Match
                      9.0%; Score 86.5; DB 2; Length 858;
 Best Local Similarity 22.7%; Pred. No. 6;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;
        18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
Qу
            117 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
Db
```

```
78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
Qγ
               168 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA 218
Db
Qу
         130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
                1 1 1
                             1111
                                         | : | |
                                               :
                                                    | | | | ::: ::|
         219 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 271
Db
Qу
         173 ---SATEIEKSISA 183
                :11:: ::1:
         272 LQDAATQLNTNLSS 285
RESULT 4
T13009
hypothetical protein T24C20.80 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 13-Aug-1999 #sequence revision 13-Aug-1999 #text change 24-Nov-1999
C; Accession: T13009
R; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.;
Artiguenave, F.; Saurin, W.; Weissenbach, J.; Mewes, H.W.; Mayer, K.F.X.;
Lemcke, K.; Schueller, C.; Quetier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, July 1999
A; Reference number: Z17586
A; Accession: T13009
A; Molecule type: DNA
A; Residues: 1-1998 < CHO>
A;Cross-references: EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.80
A; Experimental source: cultivar Columbia; BAC clone T24C20
C; Genetics:
A; Gene: ATSP: T24C20.80
A; Map position: 3
A; Introns: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; 604/1;
1005/2; 1461/3; 1791/3; 1867/1; 1914/3
C; Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80
 Query Match
                        8.7%; Score 83.5; DB 2; Length 1998;
 Best Local Similarity 29.4%; Pred. No. 27;
 Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps
Qу
          38 QRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD-EFKN--TGS 94
            1089 ERYCSA---NSALGTPSM---C------SSTGPFQDSEFENFSLGP 1122
Db
          95 GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP----KVDSDHCFPLPAM 149
Qу
             Db
        1123 SLVKLSSLDM--SRLGD----RGIHFFDEGGSCNGRSSSAPGLNTGNVNIDMCGDL--M 1173
        150 EEGATI 155
Qy
            : | | | |
Db
        1174 DGGATI 1179
RESULT 5
A57434
protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - rat
N; Alternate names: cell adhesion kinase-beta
```

```
C; Species: Rattus norvegicus (Norway rat)
C;Date: 08-Feb-1996 #sequence revision 08-Feb-1996 #text change 04-Feb-2000
C; Accession: A57434
R; Sasaki, H.; Nagura, K.; Ishino, M.; Tobioka, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1995
A; Title: Cloning and characterization of cell adhesion kinase beta, a novel
protein-tyrosine kinase of the focal adhesion kinase subfamily.
A; Reference number: A57434; MUID: 95403356; PMID: 7673154
A; Accession: A57434
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1009 <SAS>
A; Cross-references: GB:D45854; NID:g1000679; PIDN:BAA08290.1; PID:d1008885;
PID:q1000680
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein
kinase homology
C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;423-686/Domain: protein kinase homology <KIN>
F;431-439/Region: protein kinase ATP-binding motif
  Query Match
                           8.5%; Score 82; DB 2; Length 1009;
  Best Local Similarity
                          26.9%; Pred. No. 18;
  Matches 29; Conservative 13; Mismatches 34; Indels
                                                              32; Gaps
                                                                            4;
Qу
           88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                     | | :| |:|:
                                                           : |
Db
          249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDTKPTCLAEFKQI 305
Qy
          139 DSDHCFPLPAME-----EGATILVTTKTND-----YCK 166
                 | | | :
                                111
                                     :: ||:
Db
          306 RSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR 353
RESULT 6
T28669
surface protein 51C - Paramecium tetraurelia
C; Species: Paramecium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text change 07-Dec-1999
C; Accession: T28669
R; Nielsen, E.; You, Y.; Forney, J.
J. Mol. Biol. 222, 835-841, 1991
A; Title: Cysteine residue periodicity is a conserved structural feature of
variable surface proteins from Paramecium tetraurelia.
A; Reference number: Z20504; MUID: 92106337; PMID: 1762150
A; Accession: T28669
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-2233 <NIE>
A; Cross-references: EMBL: M65164; NID: g159974; PID: g159975; PIDN: AAA61740.1
C; Genetics:
A; Genetic code: SGC5
  Query Match
                          8.5%; Score 81.5; DB 2; Length 2233;
  Best Local Similarity 25.1%; Pred. No. 46;
 Matches 43; Conservative 17; Mismatches
                                                 58; Indels
                                                               53; Gaps
                                                                           10;
Qу
           6 GQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA-SVTNSVKGTNAILWTCLGLSL 64
```

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1 | | :
                           Db
         520 GSCYQKQ-----CSAASQDNTTHAQCQEYLPACTLSNTKKG----CIDLPL 561
          65 IISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDL---EKSRTGDEIILPRGLE 120
QУ
             Dh
         562 TCSA-----LIVKENCELKANREK---CGWTGSTCVDIVCTTAPTKTDD-----D 603
         121 YTVEECTC----EDCIKSKPKVDSDHCFPLPAMEEGATI----LVTTKTN 162
QУ
            Db
         604 YTVELCEAYKPSSNCV---PNGTKKGCMELAAKCESRTIKEQCDVAGTKTN 651
RESULT 7
D89010
protein R08F11.7 [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence revision 10-May-2001 #text change 17-May-2002
C; Accession: D89010
R; anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans: a platform for
investigating biology.
A; Reference number: A75000; MUID: 99069613; PMID: 9851916
A; Note: see websites genome.wustl.edu/gsc/C elegans/ and
www_sanger.ac.uk/Projects/C_elegans/ for a list of authors
A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103,
1999; and Science 285, 1493, 1999
A:Accession: D89010
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-773 <STO>
A; Cross-references: GB:chr_V; PIDN:AAB54249.1; PID:g2088832; GSPDB:GN00023;
CESP:R08F11.7
A; Note: Similar to peroxidase
C; Genetics:
A; Gene: R08F11.7
A; Map position: 5
C; Superfamily: myeloperoxidase; myeloperoxidase homology
 Query Match
                       8.4%; Score 81; DB 2; Length 773;
 Best Local Similarity 21.7%; Pred. No. 17;
 Matches 40; Conservative 25; Mismatches 91; Indels 28; Gaps
Qу
         23 PCQLRCSSNTPPLTCQ------RYCN----ASVTNSVKGTNAILWTCL---GLSL 64
            1::::
                                   111 : 111 :11
Db
        184 PPKSNATCQGPPKSCSDPVHDRIRSITGYCNNRGKPTQANSVTAIRRLLGTTSYTDGLQA 243
         65 IISLAVFVLMFLLRKISSEPLKDEFKNTG-SGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
Qу
            244 IRNTSVTGSPLPSTRLISNKLHDEGSTPNFSPSVNHLHMQIGQFIAHDIIFMPSSTAKDG 303
Db
        124 EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSA-----TE 176
Qу
              304 SSLNCTSC--SSPTTISTNCAPIPAPADDKYFTPVSRTEARCIRLTRALNGQSGFGVRTQ 361
Db
Qу
        177 IEKS 180
            1:::
```

```
RESULT 8
S60248
protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - human
N; Alternate names: cell adhesion kinase-beta
C; Species: Homo sapiens (man)
C;Date: 10-Apr-1996 #sequence revision 27-Feb-1997 #text change 17-Nov-2000
C; Accession: S60248; G02330; B57434
R; Lev, S.; Moreno, H.; Martinez, R.; Canoll, P.; Peles, E.; Musacchio, J.M.;
Plowman, G.D.; Rudy, B.; Schlessinger, J.
Nature 376, 737-745, 1995
A; Title: Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of
ion channel and MAP kinase functions.
A; Reference number: S60248; MUID: 95379967; PMID: 7544443
A; Accession: S60248
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-1009 <LEV>
A;Cross-references: EMBL:U33284; NID:g988304; PIDN:AAC50203.1; PID:g988305
R; Sasaki, T.; Nagura, K.; Sasaki, H.
submitted to the EMBL Data Library, December 1995
A; Reference number: H01067
A; Accession: G02330
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-22, 'G', 24-434, 'L', 436-1009 <SAS>
A;Cross-references: EMBL:U43522; NID:g1165218; PIDN:AAC05330.1; PID:g1165219
R; Sasaki, H.; Nagura, K.; Ishino, M.; Tobioka, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1995
A; Title: Cloning and characterization of cell adhesion kinase beta, a novel
protein-tyrosine kinase of the focal adhesion kinase subfamily.
A; Reference number: A57434; MUID: 95403356; PMID: 7673154
A; Accession: B57434
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-22, 'G', 24-150 <SA2>
A; Cross-references: GB:D45853; NID:g1000676; PIDN:BAA08289.1; PID:d1008884;
PID:g1000677
C; Genetics:
A; Gene: CAKbeta
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein
kinase homology
C; Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;423-686/Domain: protein kinase homology <KIN>
F;431-439/Region: protein kinase ATP-binding motif
  Query Match
                           8.2%; Score 79.5; DB 2; Length 1009;
  Best Local Similarity
                          32.1%; Pred. No. 31;
 Matches 25; Conservative 9; Mismatches 29; Indels
                                                                15; Gaps
                                                                             3;
          88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
Qу
                     | | :| |:|:
                                                           :
Db
          249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
         139 DSDHCFPLPAMEEGATIL 156
Qу
```

```
RESULT 9
T43251
furin (EC 3.4.21.75) - fall armyworm
N; Alternate names: paired basic amino acid cleaving enzyme; proprotein
convertase; serine proteinase PACE
C; Species: Spodoptera frugiperda (fall armyworm)
C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text change 11-Jan-2000
C; Accession: T43251
R; Cieplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A; Description: Cloning and functional characterization of FURIN from Spodoptera
frugiperda (Sf9) cells.
A; Reference number: Z22368
A; Accession: T43251
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1299 <CIE>
A; Cross-references: EMBL: Z68888; NID: g1167859; PID: e219690; PIDN: CAA93116.1
A; Experimental source: clone Sfurin 6; ovary
C; Function:
A; Description: responsible for the endoproteolytic processing of proproteins
with specificity for paired basic amino acid residues
C; Keywords: hydrolase; serine proteinase
  Query Match
                          8.2%; Score 79.5; DB 2; Length 1299;
  Best Local Similarity
                         24.1%; Pred. No. 40;
           39; Conservative 26; Mismatches
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                                                              49; Gaps
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Qу
            8 CSQNEYFDSLLHACIPCQLRCS----SNTPPLTCQRYCNAS----VTNSVKGTNAIL-W 57
                                     ::||| |:||
                    ::|| |
Db
         1150 CSRPLRIDRLNNQCVPC---CSERGVTNSTPPTDC-CHCNPENGECINSSVAGKRRIAEW 1205
           58 TCLGLS-----LIISLAV-----FVLMFLLRKISSEPLKDEFKNTGSGLLGMAN 101
QУ
               | :
                            Db
         1206 GALHTAPSADAAPSVAVVTIAVCAAAVGLFITVLVVLQAHSPREKKTRKTSVRG----- 1259
Qу
         102 IDLEKSRTGDEIILPR-GLEYTVEECTCEDCIKSKPKVDSDH 142
                     | | | | :::||
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Db
         1260 --VEYSR-----LPRTDVDFTV----LTSCTDQEGPVEYEH 1289
RESULT 10
potassium channel homolog - Methanococcus jannaschii
C; Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence revision 13-Sep-1996 #text change 21-Jul-2000
C; Accession: D64469
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.;
Blake, J.A.; FitzGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.;
Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness,
E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen,
N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley,
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J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.;
 Hurst, M.A.
 Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.;
Woese, C.R.; Venter, J.C.
A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.
A; Reference number: A64300; MUID: 96337999; PMID: 8688087
A; Accession: D64469
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-343 <BUL>
A; Cross-references: GB: U67575; GB: L77117; NID: g1591992; PIDN: AAB99365.1;
PID:g1592000; TIGR:MJ1357
C; Genetics:
A; Map position: REV1308326-1307295
C; Superfamily: conserved hypothetical protein s110993
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              : | | : | : |
                                    -:| | ::: |:|:::: |
           32 DYFTALYFSVI-----TITTTGYGDFTPKTFLGRTLTVVYLCVGVGIVMYLFSL 80
Db
           72 VLMFL-----NIDLEKSRTGD 111
Qу
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                                                             - 1-1
Db
           81 IAEFIVEGKFEEFVRLKKMKNKIKTLKDHYIICGYGRLGKVVGEKFIEENIPFIAIDINE 140
          112 EII-----DSDHCF-PLPAMEEG 152
Qу
                            | | :
                       - 1
                                   |: :| | |:
                                                          1:1: | | | |
Db
          141 DVLKEEYEKYPDKFLYIVGDAKKEEVLK-KAKIDKAKGLIATLPSDADNVFLTLTARELN 199
QУ
          153 ATILVTTKTND 163
                | | : | | : :
Db
          200 PNILITAKADE 210
RESULT 11
JC5894
killer cell inhibitory receptor p91A precursor - mouse
C; Species: Mus musculus (house mouse)
C;Date: 18-Mar-1998 #sequence revision 18-Mar-1998 #text change 17-Mar-1999
C; Accession: JC5894
R; Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa,
Y.; Ohyama, Y.; Ohmori, H.; Ono, M.; Takai, T.
J. Biochem. 123, 358-368, 1998
A; Title: Genomic structures and chromosomal location of p91, a novel murine
regulatory receptor family.
A; Reference number: JC5894; MUID: 98218758; PMID: 9538215
A; Accession: JC5894
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA
A; Residues: 1-841 <YAM>
A; Cross-references: GB: AF040946
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C; Comment: This protein function as inhibitory cell-surface molecule against
 cell activation.
 C; Genetics:
A; Map position: 7
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F;636-674/Domain: transmembrane #status predicted <TMM>
F;675-765/Domain: cytoplasmic #status predicted <CYT>
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  Best Local Similarity 22.7%; Pred. No. 35;
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Qу
                  :: : | : |
Db
          598 AQNSSFYLLSSASAPVELTVSGPIETSTPPPT-----MSMPLGGLHMYLKALIGVSV 649
Qy
           65 IISLAVFVLMFLL--RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRG--- 118
                 Db
          650 AFILFLFILIFILLRRRHRGKFRKDVQKEK------DLQLSSGAEEPITRKGELQK 699
          119 -----LEYTVEECTCEDCIK----SKPKVDSDHCFPLPAMEEGATILVTTKTN 162
Qу
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Db
          700 RPNPAAATQEESLYASVEDMQTEDGVELNSWTPPEED------PQGET----- 741
Qу
          163 DYCKSLPAAL-SATEIEKSISAR 184
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          742 -YAQVKPSRLRKAGHVSPSVMSR 763
RESULT 12
D86345
hypothetical protein F16F4.10 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text change 17-May-2002
C; Accession: D86345
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.;
Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.;
Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.;
Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etqu, P.;
Feldblyum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.;
Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.;
Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-
Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu,
S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Militscher, J.; Miranda,
M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pai, G.; Peterson, J.; Pham, P.K.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken,
S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.;
Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
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A; Status: preliminary
A; Molecule type: DNA
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C; Genetics:
A; Map position: 1
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PRO25; protein kinase homology
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          67 SLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL-----GMANIDLE 105
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             Db
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence revision 19-Feb-1999 #text change 24-Mar-1999
C; Accession: T01733
R; Scheet, P.; Maggi, L.
submitted to the EMBL Data Library, June 1997
A; Description: The sequence of A. thaliana IG002N01.
A; Reference number: Z14407
A; Accession: T01733
A; Status: translated from GB/EMBL/DDBJ
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A; Experimental source: cultivar Columbia
C; Genetics:
A; Map position: 4
A; Introns: 112/3; 136/2; 164/3; 237/3; 356/1; 430/1; 460/2; 718/2; 752/3; 781/3;
806/3; 833/3
A; Note: A IG002N01.31
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A; Accession: D86345

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147 PAMEEGATILVTTKTND----YCKSLPAALSATEIEKSISAR 184
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           873 --VPEPETVAATTTTVDKPVPEPEPVPEPVPVPAIEAAVAAQ 912
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 hypothetical protein F2K15.50 - Arabidopsis thaliana
 C; Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence revision 04-Feb-2000 #text change 20-Jun-2000
 C; Accession: T45824
R; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.;
Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.
 submitted to the Protein Sequence Database, January 2000
A; Reference number: Z23015
A; Accession: T45824
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-522 <RIE>
A; Cross-references: EMBL: AL132956
A; Experimental source: cultivar Columbia; BAC clone F2K15
C; Genetics:
A; Map position: 3
A; Introns: 69/3; 271/3; 294/1; 327/3; 397/3; 443/3
A; Note: F2K15.50
C; Superfamily: Arabidopsis thaliana hypothetical protein F2K15.70
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  Best Local Similarity
                         27.0%; Pred. No. 27;
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Qу
                   Db
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methyl-accepting chemotaxis protein - Thermotoga maritima (strain MSB8)
C; Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Accession: F72288
R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft,
D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.;
Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.;
Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.;
Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter,
J.C.; Fraser, C.M.
Nature 399, 323-329, 1999
A; Title: Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.
A; Reference number: A72200; MUID: 99287316; PMID: 10360571
A; Accession: F72288
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A; Status: preliminary A; Molecule type: DNA A; Residues: 1-539 <ARN>

A; Cross-references: GB: AE001772; GB: AE000512; NID: g4981693; PIDN: AAD36222.1;

PID:g4981694; TIGR:TM1146

A; Experimental source: strain MSB8

C; Genetics: A; Gene: TM1146

C; Superfamily: methyl-accepting chemotaxis protein

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Qу 99 MANIDLEKSRTGDEI 113

Db 203 --NVEIEKIRSKDEI 215

Search completed: April 19, 2004, 13:23:35

Job time : 12.2222 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:21:03; Search time 28.7737 Seconds

(without alignments)

1762.857 Million cell updates/sec

Title: PCT-US03-05147-1

Perfect score:

Sequence: 1 MLQMAGQCSQNEYFDSLLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

1124875 seqs, 275673149 residues Searched:

Total number of hits satisfying chosen parameters: 1124875

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query

> No. Score Match Length DB ID

Description

1	964	100.0	184	13	US-10-077-438-1	Sequence 1, Appli
2	964	100.0	184	13		Sequence 7, Appli
3	964	100.0	184	13		Sequence 1, Appli
4	964	100.0	184	13		Sequence 7, Appli
5	964	100.0	184	14		Sequence 2, Appli
6	964	100.0	184	14		Sequence 47, Appl
7	964	100.0	184	14		Sequence 8, Appli
8	964	100.0	184	14		Sequence 7, Appli
9	964	100.0	184	14		Sequence 27, Appli
10	964	100.0	184	14		Sequence 11, Appl
11	964	100.0	184	15		Sequence 39, Appl
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13	950	98.5	181	12		Sequence 5, Appli
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16	572	59.3	185	14		Sequence 17, Appl
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19	311.5	32.3	117	9	US-09-854-864-12	Sequence 12, Appl
20	311.5	32.3	117	12	US-09-855-158-12	Sequence 12, Appl
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36	104	10.8	21	9	US-09-854-864-8	Sequence 8, Appli
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40	93	9.6	184	14	US-10-008-063-2	Sequence 2, Appli
41	93	9.6	184	14	US-10-152-363A-60	Sequence 60, Appl
42	91	9.4	171	14	US-10-251-947-4	Sequence 4, Appli
43	91	9.4	171	14	US-10-251-947-7	Sequence 7, Appli
44	90.5	9.4	170	14	US-10-251-947-6	Sequence 6, Appli
45	86.5	9.0	392	14	US-10-152-363A-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1 US-10-077-438-1

- ; Sequence 1, Application US/10077438
- ; Publication No. US20020165156A1
- ; GENERAL INFORMATION:
- ; APPLICANT: MacKay, Fabienne

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APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
  APPLICANT: Schneider, Pascal
  APPLICANT: Thompson, Jeffrey
  APPLICANT: Biogen, Inc.
  APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
  PRIOR APPLICATION NUMBER: 60/149,378
 PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
   LENGTH: 184
   TYPE: PRT
   ORGANISM: homo sapien
US-10-077-438-1
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            Db
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; Publication No. US20020165156A1
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; APPLICANT: MacKay, Fabienne
 APPLICANT: Browning, Jeffrey
 APPLICANT: Ambrose, Christine APPLICANT: Tschopp, Jurg
  APPLICANT: Schneider, Pascal
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APPLICANT: Thompson, Jeffrey
  APPLICANT: Biogen, Inc.
  APPLICANT: Apotech R&D S.A.
  TITLE OF INVENTION: Baff Receptor (BCMA), An
  TITLE OF INVENTION: Immunoregulatory Agent
  FILE REFERENCE: A080PCT
  CURRENT APPLICATION NUMBER: US/10/077,438
  CURRENT FILING DATE: 2002-02-18
  PRIOR APPLICATION NUMBER: 60/149,378
 PRIOR FILING DATE: 1999-08-17
 PRIOR APPLICATION NUMBER: 60/181,684
  PRIOR FILING DATE: 2000-02-11
  PRIOR APPLICATION NUMBER: 60/183,536
 PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
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; SEQ ID NO 7
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   TYPE: PRT
   ORGANISM: homo sapien
US-10-077-438-7
  Query Match
                       100.0%; Score 964; DB 13; Length 184;
 Best Local Similarity 100.0%; Pred. No. 6.6e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels
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Qу
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            Db
          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
            Db
         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
        121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
            121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db
        181 ISAR 184
Qу
            181 ISAR 184
Db
RESULT 3
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
 APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
 APPLICANT: Schneider, Pascal
  APPLICANT: Thompson, Jeffrey
  APPLICANT: Biogen, Inc.
  APPLICANT: Apotech R&D S.A.
  TITLE OF INVENTION: Baff Receptor (BCMA), An
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TITLE OF INVENTION: Immunoregulatory Agent
   FILE REFERENCE: A080PCT
   CURRENT APPLICATION NUMBER: US/10/077,137
   CURRENT FILING DATE: 2001-02-15
   PRIOR APPLICATION NUMBER: 60/149,378
   PRIOR FILING DATE: 1999-08-17
   PRIOR APPLICATION NUMBER: 60/181,684
  PRIOR FILING DATE: 2000-02-11
  PRIOR APPLICATION NUMBER: 60/183,536
  PRIOR FILING DATE: 2000-02-18
  NUMBER OF SEQ ID NOS: 8
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 1
   LENGTH: 184
   TYPE: PRT
    ORGANISM: homo sapien
US-10-077-137-1
  Query Match
                       100.0%; Score 964; DB 13;
                                                 Length 184;
  Best Local Similarity
                       100.0%; Pred. No. 6.6e-94;
  Matches 184; Conservative 0; Mismatches
                                           0; Indels
                                                          0;
                                                              Gaps
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Qу
             Db
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          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
             Db
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qy
            Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
         181 ISAR 184
QУ
            Db
         181 ISAR 184
RESULT 4
US-10-077-137-7
; Sequence 7, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
  APPLICANT: MacKay, Fabienne
  APPLICANT: Browning, Jeffrey
  APPLICANT: Ambrose, Christine
  APPLICANT: Tschopp, Jurg
  APPLICANT: Schneider, Pascal
  APPLICANT: Thompson, Jeffrey
  APPLICANT: Biogen, Inc.
  APPLICANT: Apotech R&D S.A.
  TITLE OF INVENTION: Baff Receptor (BCMA), An
  TITLE OF INVENTION: Immunoregulatory Agent
  FILE REFERENCE: A080PCT
  CURRENT APPLICATION NUMBER: US/10/077,137
  CURRENT FILING DATE: 2001-02-15
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PRIOR APPLICATION NUMBER: 60/149,378
  PRIOR FILING DATE: 1999-08-17
  PRIOR APPLICATION NUMBER: 60/181,684
  PRIOR FILING DATE: 2000-02-11
  PRIOR APPLICATION NUMBER: 60/183,536
  PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
   LENGTH: 184
    TYPE: PRT
    ORGANISM: homo sapien
US-10-077-137-7
                       100.0%; Score 964; DB 13; Length 184;
  Query Match
  Best Local Similarity 100.0%; Pred. No. 6.6e-94;
  Matches 184; Conservative 0; Mismatches
                                            0; Indels
                                                          0; Gaps
                                                                     0;
Qу
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
            Db
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
             61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
            Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
         181 ISAR 184
Qv
            Db
         181 ISAR 184
RESULT 5
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
  APPLICANT: Kindsvogel, Wayne
  TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
  FILE REFERENCE: 01-04
  CURRENT APPLICATION NUMBER: US/10/068,725
  CURRENT FILING DATE: 2002-02-06
  PRIOR APPLICATION NUMBER: 60/270,274
  PRIOR FILING DATE: 2001-02-20
  PRIOR APPLICATION NUMBER: 60/283,447
  PRIOR FILING DATE: 2001-04-12
  NUMBER OF SEQ ID NOS: 5
  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
   LENGTH: 184
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-068-725-2
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Query Match
                     100.0%; Score 964; DB 14; Length 184;
  Best Local Similarity 100.0%; Pred. No. 6.6e-94;
  Matches 184; Conservative 0; Mismatches 0; Indels
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                                                                0;
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            Db
          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
            Db
         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
        121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qv
            Db
        121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
        181 ISAR 184
QУ
           Db
        181 ISAR 184
RESULT 6
US-10-151-882-47
; Sequence 47, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
  TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
  FILE REFERENCE: PF554
 CURRENT APPLICATION NUMBER: US/10/151.882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
   LENGTH: 184
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-151-882-47
                    100.0%; Score 964; DB 14; Length 184;
 Query Match
 Best Local Similarity 100.0%; Pred. No. 6.6e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels
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Qу
           Db
          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
           61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Db
        121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
           121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Db
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Db
         181 ISAR 184
RESULT 7
US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
  APPLICANT: Biogen, Inc.
  TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
  FILE REFERENCE: A083PCT
  CURRENT APPLICATION NUMBER: US/10/115,192
  CURRENT FILING DATE: 2002-04-02
  PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
  PRIOR APPLICATION NUMBER: 60/181807
  PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
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   TYPE: PRT
   ORGANISM: homo sapiens
US-10-115-192-8
 Query Match
                       100.0%; Score 964; DB 14; Length 184;
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 Matches 184; Conservative 0; Mismatches 0;
                                               Indels
                                                         0; Gaps
                                                                    0;
Qy
          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
            Db
          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
QУ
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
            Dh
         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
        121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
            Db
        121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
        181 ISAR 184
QУ
            Db
        181 ISAR 184
RESULT 8
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
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QУ

181 ISAR 184

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; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
 FILE REFERENCE: 00-103
  CURRENT APPLICATION NUMBER: US/10/008,063
  CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
   LENGTH: 184
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-008-063-7
  Query Match
                       100.0%; Score 964; DB 14; Length 184;
  Best Local Similarity 100.0%; Pred. No. 6.6e-94;
  Matches 184; Conservative 0; Mismatches 0; Indels
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                                                                    0;
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QУ
            Db
          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
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Qу
            Db
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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            Db
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        181 ISAR 184
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            Db
        181 ISAR 184
RESULT 9
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
  APPLICANT: Gross, Jane A.
 TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
 FILE REFERENCE: 01-20
  CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
  PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
 SOFTWARE: FastSEQ for Windows Version 3.0
; SEO ID NO 27
  LENGTH: 184
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-152-363A-27
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Query Match
                      100.0%; Score 964; DB 14; Length 184;
  Best Local Similarity 100.0%; Pred. No. 6.6e-94;
  Matches 184; Conservative
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                                           0;
                                              Indels
                                                          Gaps
                                                                  0;
Qу
           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
            1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Db
          61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
            61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
            Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
         181 ISAR 184
QУ
            Db
         181 ISAR 184
RESULT 10
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
  APPLICANT: Shu, Hong-Bing
  TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
  TITLE OF INVENTION: METHODS OF USE THEREOF
  FILE REFERENCE: 2879-72
  CURRENT APPLICATION NUMBER: US/10/216,074
  CURRENT FILING DATE: 2003-03-12
  PRIOR APPLICATION NUMBER: US/09/565,423
  PRIOR FILING DATE: 2000-05-05
  PRIOR APPLICATION NUMBER: UNKNOWN
  PRIOR FILING DATE: 2000-05-01
  PRIOR APPLICATION NUMBER: 60/132,892
  PRIOR FILING DATE: 1999-05-06
  NUMBER OF SEO ID NOS: 17
  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
   LENGTH: 184
   TYPE: PRT
   ORGANISM: Homo sapiens
US-10-216-074-11
 Query Match
                      100.0%; Score 964; DB 14;
                                              Length 184;
 Best Local Similarity 100.0%; Pred. No. 6.6e-94;
 Matches 184; Conservative 0; Mismatches 0; Indels
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                                                                 0;
                                                          Gaps
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Qу
            1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
Db
         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
Qу
            Db
         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
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121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Qу
             121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Db
Qу
         181 ISAR 184
             \mathbf{H}
Db
         181 ISAR 184
RESULT 11
US-10-087-080-39
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
  TITLE OF INVENTION: No. US20030235820Alel Methods of Diagnosis of Metastatic
Colorectal
  TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
  TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
  PRIOR APPLICATION NUMBER: US 60/272,206
  PRIOR FILING DATE: 2001-02-27
  PRIOR APPLICATION NUMBER: US 60/281,149
  PRIOR FILING DATE: 2001-04-02
  PRIOR APPLICATION NUMBER: US 60/284,555
  PRIOR FILING DATE: 2001-04-17
 NUMBER OF SEQ ID NOS: 41
  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
   LENGTH: 184
   TYPE: PRT
;
   ORGANISM: Homo sapiens
   FEATURE:
   OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
   OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39
  Query Match
                       100.0%; Score 964; DB 15; Length 184;
 Best Local Similarity 100.0%; Pred. No. 6.6e-94;
 Matches 184; Conservative
                            0; Mismatches
                                           0; Indels
                                                         0;
                                                                    0;
Qу
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            Db
          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
QУ
            Db
         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
        121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
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Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
Qу
         181 ISAR 184
            ++++
Db
         181 ISAR 184
RESULT 12
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
  APPLICANT: THEILL, LARS EYDE
  APPLICANT: YU, GANG
 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA.
  TITLE OF INVENTION: BLYS/AGP-3, AND TACI
  FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
 PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
   LENGTH: 181
   TYPE: PRT
   ORGANISM: Homo sapiens
US-09-854-864-5
 Query Match
                      98.5%; Score 950; DB 9; Length 181;
 Best Local Similarity 100.0%; Pred. No. 2e-92;
 Matches 181; Conservative 0; Mismatches 0; Indels
                                                                    0;
Qу
          4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
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Db
         64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
Qу
            Db
         61 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV 120
        124 EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
QУ
            Db
        121 EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180
        184 R 184
Qу
Db
        181 R 181
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RESULT 13

US-09-855-158-5

[;] Sequence 5, Application US/09855158

[;] Publication No. US20020086018A1

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; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA, BLYS/AGP-
  TITLE OF INVENTION: 3, AND TACI
   FILE REFERENCE: A-686A
  CURRENT APPLICATION NUMBER: US/09/855,158
  CURRENT FILING DATE: 2001-09-11
  PRIOR APPLICATION NUMBER: US 60/214,591
  PRIOR FILING DATE: 2000-06-27
  PRIOR APPLICATION NUMBER: US 60/204,039
  PRIOR FILING DATE: 2000-05-12
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn version 3.1
; SEO ID NO 5
   LENGTH: 181
   TYPE: PRT
   ORGANISM: Homo sapiens
US-09-855-158-5
  Query Match
                       98.5%; Score 950; DB 12; Length 181;
  Best Local Similarity 100.0%; Pred. No. 2e-92;
  Matches 181; Conservative 0; Mismatches
                                           0; Indels
                                                                     0:
Qy
           4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
            Db
           1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 60
Qу
          64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
            Db
          61 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV 120
         124 EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
Qу
            121 EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180
Db
Qу
        184 R 184
Db
        181 R 181
RESULT 14
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
 APPLICANT: YU, GANG
  TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
 CURRENT FILING DATE: 2001-09-11
  PRIOR APPLICATION NUMBER: US 60/204,039
  PRIOR FILING DATE: 2000-05-12
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PRIOR APPLICATION NUMBER: US 60/214,591
   PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 31
  SOFTWARE: PatentIn version 3.1
 ; SEO ID NO 11
    LENGTH: 185
    TYPE: PRT
    ORGANISM: Murine
US-09-854-864-11
  Query Match
                        59.3%; Score 572; DB 9; Length 185;
  Best Local Similarity 62.6%; Pred. No. 2.3e-52;
  Matches 117; Conservative 21; Mismatches 41; Indels
                                                                     4;
           4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
Qу
             Db
           1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58
          64 LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
Qу
             59 LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL 118
Db
         120 EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Qу
             119 EYTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALQSVMGM 178
Db
Qу
         178 EKSISAR 184
             Db
         179 EKPTHTR 185
RESULT 15
US-09-855-158-11
; Sequence 11, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
  APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
 TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
BCMA, BLYS/AGP-
  TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
  CURRENT APPLICATION NUMBER: US/09/855,158
  CURRENT FILING DATE: 2001-09-11
  PRIOR APPLICATION NUMBER: US 60/214,591
  PRIOR FILING DATE: 2000-06-27
  PRIOR APPLICATION NUMBER: US 60/204,039
  PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
   LENGTH: 185
   TYPE: PRT
   ORGANISM: Murine
US-09-855-158-11
```

		Similarity 62.6%; Pred. No. 2.3e-52;
Matches	11	7; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
Qу	4	MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
Db	1	:
QУ	64	LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGL 119
Db	59	:: : : :: ::
QУ	120	EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
Db	119	
Qу	178	EKSISAR 184
Db	179	EKPTHTR 185

Search completed: April 19, 2004, 13:25:47 Job time: 28.7737 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:17:32; Search time 27.2593 Seconds

(without alignments)

2129.748 Million cell updates/sec

Title: PCT-US03-05147-1

Perfect score: 964

Sequence: 1 MLQMAGQCSQNEYFDSLLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp archea:*

2: sp bacteria:*

3: sp fungi:*

4: sp_human:*

5: sp invertebrate:*

6: sp mammal:*

7: sp mhc:*

8: sp organelle:*

9: sp phage:*

10: sp_plant:*

11: sp_rodent:*
12: sp_virus:*

13: sp vertebrate:*

14: sp unclassified:*

15: sp rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

용

Result Query

No. Score Match Length DB ID

Description

1	116.5	12.1	175	11	00D4W0	
2	92.5	9.6	334	11 2	Q8R4W8 Q8GM90	Q8r4w8 mus musculu
3	88.5	9.2	217	16	~	Q8gm90 symbiont ba
4	86.5	9.0	804	11	~	Q97d61 clostridium
5	86.5	9.0	809	11	~	Q80xb3 mus musculu
6	86.5	9.0	823	11	2	Q80xb2 mus musculu
7	86.5	9.0	827	11	£	Q80xb6 mus musculu
8	86.5	9.0	834	11	2 110	Q8cdk8 mus musculu
9	86.5	9.0	842	11	~	Q8bh12 mus musculu
10	85.5	8.9	1193	5	Q0K036	Q8r056 mus musculu
11	83.5	8.7	938	10	_	Q9y1x8 ephydatia f
12	83.5	8.7	1998	10	~	Q8rwv7 arabidopsis
13	83	8.6	449	11	~	Q9str8 arabidopsis
14	83	8.6	474	11	~	Q8c6r5 mus musculu
15	82	8.5	327	6	097491	Q8c914 mus musculu
16	82	8.5	967	11		097491 ovis aries
17	81.5	8.5	314	11	Q8VEV6	Q8c2g0 mus musculu
18	81.5	8.5	2233	5	094711	Q8vev6 mus musculu
19	81	8.4	595	10	~	Q94711 paramecium
20	81	8.4	773	5	Q39191 O01892	Q39191 arabidopsis
21	80.5	8.4	314	11		001892 caenorhabdi
22	80.5	8.4	487	5	Q71QQ9 Q8IN99	Q7tqq9 mus musculu
23	80	8.3	735	10	O81820	Q8in99 drosophila
24	79.5	8.2	153	2	Q8KLY1	081820 arabidopsis
25	79.5	8.2	1299	5	Q26489	Q8kly1 pseudomonas
26	79.3	8.2	1200	13	_	Q26489 spodoptera
27	78.5	8.1	314	11	Q802S1 Q8VFW0	Q802s1 fugu rubrip
28	78.5	8.1	485	4	Q9H677	Q8vfw0 mus musculu
29	78.5	8.1	522	4	Q8N6T0	Q9h677 homo sapien
30	78.5	8.1	789	10	Q8LQ43	Q8n6t0 homo sapien
31	78	8.1	841	11	Q8R2Z1	Q8lq43 oryza sativ
32	77.5	8.0	738	10	Q9LMN6	Q8r2z1 mus musculu
33	77.5	8.0	738	10	081819	Q9lmn6 arabidopsis
34	77.5	8.0	853	15	Q9YKU7	081819 arabidopsis
35	77.5	8.0	968	10	004623	Q9yku7 human immun
36	77	8.0	522	10	Q9M3B3	004623 arabidopsis
37	77	8.0	539	16	Q9X0N0	Q9m3b3 arabidopsis
38	76.5	7.9	357	5	Q9XV87	Q9x0n0 thermotoga
39	76.5	7.9	656	10	Q9FJE3	Q9xv87 caenorhabdi
40	76.5	7.9	1404	5	045251	Q9fje3 arabidopsis
41	76	7.9	797	3	Q872A6	045251 caenorhabdi
42	76	7.9	1805	11	Q63661	Q872a6 neurospora
43	75.5	7.8	202	16	Q8D6L4	Q63661 rattus norv
44	75.5	7.8	567	12	Q8JKV7	Q8d614 vibrio vuln
45	75.5	7.8	450	16	Q97E85	Q8jkv7 heliothis z
	, 5	, • 0	100	10	Z21E02	Q97e85 clostridium

ALIGNMENTS

```
RESULT 1
Q8R4W8

ID Q8R4W8 PRELIMINARY; PRT; 175 AA.

AC Q8R4W8;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
```

```
TRAF3 binding protein.
 DΕ
     TNFRSF13C.
 GN
OS
     Mus musculus (Mouse).
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
     NCBI TaxID=10090;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RA
     Mizuno K., Irie S., Sato T.-A.;
     "Identification of novel TRAF3 binding protein, T3BP, which increases
RT
     cellular F-actin content.";
RT
RL
     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR
     EMBL; AF350257; AAL83914.1; -.
DR
     MGD; MGI:1919299; Tnfrsf13c.
     SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;
SQ
  Query Match
                        12.1%; Score 116.5; DB 11; Length 175;
  Best Local Similarity 29.4%; Pred. No. 0.00049;
  Matches
          50; Conservative 21; Mismatches 64; Indels 35; Gaps
Qy
           7 QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
             Db
          21 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80
Qу
          57 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111
                : |: : | |
Db
          81 GLILALTLVGLVSLVSWRWRQQLRTASPDTSEGVQQE-----SLENVFVPSSET-- 129
Qу
         112 EIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT 161
                          Db
         130 ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSTELVTTKT 170
RESULT 2
Q8GM90
ID
     Q8GM90
               PRELIMINARY; PRT; 334 AA.
AC
     Q8GM90;
DT
    01-MAR-2003 (TrEMBLrel. 23, Created)
    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
   Putative acyltransferase.
GN
    PEDC.
OS
    symbiont bacterium of Paederus fuscipes.
OC
    Bacteria.
OX
    NCBI TaxID=176282;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RX
    MEDLINE=22294974; PubMed=12381784;
RA
    Piel J.;
RT
    "A polyketide synthase-peptide synthetase gene cluster from an
RT
    uncultured bacterial symbiont of Paederus beetles.";
RL
    Proc. Natl. Acad. Sci. U.S.A. 99:14002-14007(2002).
    EMBL; AY059471; AAL27848.1; -.
DR
    GO; GO:0008415; F:acyltransferase activity; IEA.
DR
    GO; GO:0016740; F:transferase activity; IEA.
DR
DR
    GO; GO:0008152; P:metabolism; IEA.
DR
    InterPro; IPR001227; Ac trans.
```

```
Pfam; PF00698; Acyl transf; 1.
KW
     Transferase; Acyltransferase.
     SEQUENCE 334 AA; 38018 MW; 6C42D1FFEC5E35F3 CRC64;
SQ
  Query Match
                         9.6%; Score 92.5; DB 2; Length 334;
  Best Local Similarity 25.0%; Pred. No. 0.33;
          42; Conservative 22; Mismatches 65; Indels 39; Gaps
                                                                      7:
          14 FDSLLHACIPCQLRCSSNTPPLTCQRYCNAS--VTNSVKGTNAILWTCLGLSLIISLA-- 69
Qу
                     11 1:1
Db
          72 FDRLIH-----THPALFMVQYALAKSLLARGLPAPDFLIGASLGEFIAISLAGD 120
          70 VFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCE 129
Qν
               Db
         121 THVENILFNLIKQARLFDEYCNAGAMLLVIDHID-----TFSTTPAFSK 164
         130 DCIKSKPKVDSDHCFPLPAMEEGATILVT----TKTNDYCKSLPAALS 173
QУ
             Db
         165 DC--ELAGINFDHCFVVSGPRTG--ILQTRKSLTKQNIACQLLPVSIA 208
RESULT 3
Q97D61
    Q97D61
               PRELIMINARY; PRT;
                                      217 AA.
    Q97D61;
AC
    01-OCT-2001 (TrEMBLrel. 18, Created)
DT
DT
    01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
    01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT
DE
    Amino acid ABC transporter, permease component.
GN
    CAC3619.
OS
    Clostridium acetobutylicum.
OC
    Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC
    Clostridium.
OX
    NCBI TaxID=1488;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX
    MEDLINE=21359325; PubMed=11466286;
RA
    Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA
    Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA
    Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA
    Bennett G.N., Koonin E.V., Smith D.R.;
RT
    "Genome sequence and comparative analysis of the solvent-producing
RT
    bacterium Clostridium acetobutylicum.";
    J. Bacteriol. 183:4823-4838(2001).
RL
    EMBL; AE007858; AAK81542.1; -.
DR
    PIR; C97344; C97344.
DR
    GO; GO:0016020; C:membrane; IEA.
    GO; GO:0005215; F:transporter activity; IEA.
DR
DR
    GO; GO:0006810; P:transport; IEA.
DR
    InterPro; IPR000515; BPD transp.
    Pfam; PF00528; BPD transp; 1.
DR
    PROSITE; PS00402; BPD TRANSP INN MEMBR; 1.
KW
    Complete proteome.
             217 AA; 23743 MW; 36738BCDC0DE8A2F CRC64;
SQ
    SEQUENCE
 Query Match
                        9.2%; Score 88.5; DB 16; Length 217;
```

DR

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Best Local Similarity 24.8%; Pred. No. 0.52;
     Matches 55; Conservative 25; Mismatches 77; Indels 65; Gaps
                     16 SLLHACIPCQLRCSSNTPPLTCQRYCNASV----TNSVKGTNAI----LWTCLGL 62
  Qу
                          4 SSLNKVIPVLLDGTRITLLLTCSSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT 63
  Db
                     63 SLIISLAVFV--LMFLLRKISSEPLKDEF----KNTGS-----GLLGMANIDLEKSR 108
  Qу
                            ]:: | ]: | [] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:] | [:]
                     64 PLLLQLYVYYYGLPFLSDKLTMTPMKAAILGLSLNSGAYIAEIIRGGILAIDNGQFEASK 123
  Db
                   109 -----TGDEIILPRGLEYTVEEC-----TCEDCI-KSKPKVDSDH 142
 Qу
                                         1 1111: : : [
                                                                                                       1 1: : 1:: 1 1
                   124 ALGLTYGQTMKRIILPQAIRVVIPPCGNEFIAMIKDTSLVSVITMEELLRKAQLLVSSSG 183
 Db
                  143 CFPLPAMEEGA--TILVTTKTNDYCKSLPAALSATEIEKSIS 182
 Qу
                                                 | : |
 Db
                   184 DAVTPYLFAGIFYLILTTIFTGIFSK-----IEKKLS 215
 RESULT 4
 Q80XB3
 ID
         Q80XB3
                            PRELIMINARY; PRT; 804 AA.
 AC
         Q80XB3;
 DT
          01-JUN-2003 (TrEMBLrel. 24, Created)
         01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
         01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE
         Prominin-1 T2 isoform.
 GN
         PROM1.
 OS
         Mus musculus (Mouse).
OC
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
         NCBI TaxID=10090;
RN
         [1]
RP
         SEQUENCE FROM N.A.
         STRAIN=BALB/c; TISSUE=Testis;
RC
RA
         Fargeas C.A., Huttner W.B., Corbeil D.;
         "Identification and characterization of a mouse prominin-1 splice
RT
RT
         variant.";
RL
         Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
        EMBL; AY223521; AA072429.1; -.
        GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR
DR
        GO; GO:0005488; F:binding; IEA.
DR
        GO; GO:0006810; P:transport; IEA.
DR
        InterPro; IPR001993; Mitoch carrier.
DR
        PROSITE; PS00215; MITOCH CARRIER; 1.
SQ
        SEQUENCE 804 AA; 89983 MW; CFC9D6E8BCF9FF16 CRC64;
   Query Match
                                              9.0%; Score 86.5; DB 11; Length 804;
    Best Local Similarity 22.7%; Pred. No. 3.9;
   Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;
Qу
                   18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
                        112 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 162
                   78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
Qу
```

```
:::: : | |
                                  163 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA 213
Db
         130 ----DCIKS-----KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
QУ
             214 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 266
Db
Qу
         173 ---SATEIEKSISA 183
               :||:: ::|:
Db
         267 LQDAATQLNTNLSS 280
RESULT 5
080XB2
ID
    Q80XB2
             PRELIMINARY; PRT; 809 AA.
AC:
    O80XB2;
DT
    01-JUN-2003 (TrEMBLrel. 24, Created)
DT
    01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
    Prominin-1 T3 isoform.
GN
    PROM1.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=BALB/c; TISSUE=Testis;
RA
    Fargeas C.A., Huttner W.B., Corbeil D.;
RT
    "Identification and characterization of a mouse prominin-1 splice
RT
    variant.":
    Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RL
    EMBL; AY223522; AA072430.1; -.
DR
    GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR
DR
    GO; GO:0005488; F:binding; IEA.
DR
    GO; GO:0006810; P:transport; IEA.
    InterPro; IPR001993; Mitoch carrier.
DR
DR
    PROSITE; PS00215; MITOCH CARRIER; 1.
    SEQUENCE 809 AA; 90605 MW; BC991E100C623AE1 CRC64;
SQ
 Query Match
                       9.0%; Score 86.5; DB 11; Length 809;
 Best Local Similarity 22.7%; Pred. No. 3.9;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps
         18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
Qу
            Db
        117 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
Qy
         78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
              168 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA 218
Db
        130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
Qγ
               1 1
                            | : | | | | ::: ::|
        219 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 271
Db
Qу
        173 ---SATEIEKSISA 183
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```
RESULT 6
Q80XB6
                              PRT; 823 AA.
               PRELIMINARY;
   Q80XB6
ID
    Q80XB6;
AC
    01-JUN-2003 (TrEMBLrel. 24, Created)
    01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DT
    Prominin T4 isoform.
DE
    PROM.
GN
    Mus musculus (Mouse).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
    NCBI TaxID=10090;
OX
RN
    [1]
    SEQUENCE FROM N.A.
RP
     STRAIN=BALB/c; TISSUE=Testis;
RC
    Fargeas C.A., Huttner W.B., Corbeil D.;
RA
    "Identification and characterization of a novel mouse prominin isoform
RT
     with an alternative C-terminal domain.";
RT
    Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RL
    EMBL; AY099088; AAM28245.1; -.
DR
    GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR
     GO; GO:0005488; F:binding; IEA.
DR
    GO; GO:0006810; P:transport; IEA.
DR
     InterPro; IPR001993; Mitoch carrier.
DR
     PROSITE; PS00215; MITOCH CARRIER; 1.
     SEQUENCE 823 AA; 92225 MW; 9EF01A18DB84EFAC CRC64;
SQ
                        9.0%; Score 86.5; DB 11; Length 823;
  Query Match
  Best Local Similarity 22.7%; Pred. No. 4;
  Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;
          18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
 Qу
                                                  117 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
 Db
           78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
 Qу
               168 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA 218
 Db
          130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
 QУ
                 111 1:11 : 111 ::::::
          219 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 271
 Db
          173 ---SATEIEKSISA 183
 QУ
                :||:: ::|:
          272 LQDAATQLNTNLSS 285
 Db
 RESULT 7
 Q8CDK8
               PRELIMINARY; PRT; 827 AA.
     Q8CDK8
 ID
      O8CDK8;
 АC
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01-MAR-2003 (TrEMBLrel. 23, Created)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DT
DE
    Prominin.
    PROM1 OR 4932416E19RIK.
GN
    Mus musculus (Mouse).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
    NCBI TaxID=10090;
OX
RN
    [1]
    SEQUENCE FROM N.A.
RΡ
    STRAIN=C57BL/6J; TISSUE=Testis;
RC
    MEDLINE=22354683; PubMed=12466851;
RX
    The FANTOM Consortium,
RA
    the RIKEN Genome Exploration Research Group Phase I & II Team;
RA
     "Analysis of the mouse transcriptome based on functional annotation of
RT
     60,770 full-length cDNAs.";
RT
    Nature 420:563-573(2002).
RL
    EMBL; AK029921; BAC26678.1; -.
DR
    MGD; MGI:1100886; Prom1.
    GO; GO:0005903; C:brush border; IDA.
DR
    GO; GO:0005887; C:integral to plasma membrane; IDA.
DR
    GO; GO:0005902; C:microvillus; IDA.
DR
     InterPro; IPR001993; Mitoch carrier.
DR
    InterPro; IPR008795; Prominin.
DR
     Pfam; PF05478; Prominin; 1.
DR
     PROSITE; PS00215; MITOCH CARRIER; 1.
DR
     SEQUENCE 827 AA; 92715 MW; DBCA5ED2DF401A18 CRC64;
SQ
                         9.0%; Score 86.5; DB 11; Length 827;
  Query Match
  Best Local Similarity 22.7%; Pred. No. 4;
          44; Conservative 30; Mismatches 67; Indels 53; Gaps
          18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
Qу
             117 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
Db
          78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
QУ
                                     | | | | | | : : | | | : : : | | | : |
               :::: : | |
         168 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA 218
Db
         130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
QУ
                               219 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 271
Db
         173 ---SATEIEKSISA 183
QУ
                :||:: ::|:
Db
         272 LQDAATQLNTNLSS 285
RESULT 8
Q8BH12
                PRELIMINARY; PRT; 834 AA.
ID
     Q8BH12
AC
     Q8BH12;
     01-MAR-2003 (TrEMBLrel. 23, Created)
DT
     01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DТ
     01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DT
```

```
DE
    Prominin T1 isoform.
GN
    PROM1 OR 4932416E19RIK.
OS
    Mus musculus (Mouse).
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=BALB/c; TISSUE=Testis;
RA
    Fargeas C.A., Huttner W.B., Corbeil D.;
RT
    "Identification and characterization of a mouse prominin isoform.";
RL
    Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN
    [2]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=C57BL/6J; TISSUE=Testis;
RX
    MEDLINE=22354683; PubMed=12466851;
RA
    The FANTOM Consortium,
RA
    the RIKEN Genome Exploration Research Group Phase I & II Team;
RT
    "Analysis of the mouse transcriptome based on functional annotation of
    60,770 full-length cDNAs.";
RT
    Nature 420:563-573(2002).
RL
    EMBL; AF305215; AA011840.1; -.
DR
DR
    EMBL; AK030027; BAC26745.1; -.
DR
    MGD; MGI:1100886; Prom1.
    GO; GO:0005903; C:brush border; IDA.
DR
    GO; GO:0005887; C:integral to plasma membrane; IDA.
DR
DR
    GO; GO:0005902; C:microvillus; IDA.
DR
    InterPro; IPR001993; Mitoch carrier.
DR
    InterPro; IPR008795; Prominin.
    Pfam; PF05478; Prominin; 1.
DR
    PROSITE; PS00215; MITOCH CARRIER; 1.
SO
    SEQUENCE 834 AA; 93444 MW; 5ABA26C80F636E45 CRC64;
 Query Match
                        9.0%; Score 86.5; DB 11; Length 834;
 Best Local Similarity 22.7%; Pred. No. 4.1;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps
                                                                      10;
          18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
Qу
                              1:1:1
            11||||:: : : : :
         117 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
Db
          78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
Qу
              Db
         168 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA 218
         130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
Qу
                Db
         219 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 271
         173 ---SATEIEKSISA 183
Qу
               :||:: ::|:
Db
         272 LQDAATQLNTNLSS 285
RESULT 9
Q8R056
ID
   Q8R056
              PRELIMINARY; PRT; 842 AA.
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AС
    Q8R056;
DT
    01-JUN-2002 (TrEMBLrel. 21, Created)
DT
    01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
    Hypothetical protein.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Eye;
RA
    Strausberg R.;
RT.
    Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; BC028286; AAH28286.1; -.
DR
    GO; GO:0005743; C:mitochondrial inner membrane; IEA.
    GO; GO:0005488; F:binding; IEA.
DR
    GO; GO:0006810; P:transport; IEA.
    InterPro; IPR001993; Mitoch carrier.
DR
DR
    InterPro; IPR008795; Prominin.
DR
    Pfam; PF05478; Prominin; 1.
DR
    PROSITE; PS00215; MITOCH CARRIER; 1.
KW
    Hypothetical protein.
SQ
    SEQUENCE 842 AA; 94478 MW; 734C10D715E5BC92 CRC64;
 Query Match
                        9.0%; Score 86.5; DB 11; Length 842;
 Best Local Similarity 22.7%; Pred. No. 4.1;
         44; Conservative 30; Mismatches 67; Indels 53; Gaps
                                                                      10;
          18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
Qу
             Db
         126 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 176
          78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
QУ
              Db
         177 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA 227
         130 ----DCIKS-----KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
Qу
                | | : | | | | | ::: ::|
Db
         228 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 280
         173 ---SATEIEKSISA 183
Qу
               :||:: ::|:
Db
         281 LQDAATQLNTNLSS 294
RESULT 10
Q9Y1X8
ID
    Q9Y1X8
               PRELIMINARY; PRT; 1193 AA.
АC
    Q9Y1X8;
    01-NOV-1999 (TrEMBLrel. 12, Created)
    01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
   Protein tyrosine kinase.
GN
    EFPTK178.
OS
    Ephydatia fluviatilis.
    Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
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OC
     Haplosclerida; Spongillidae; Ephydatia.
OX
     NCBI TaxID=31330;
RN
RP
     SEQUENCE FROM N.A.
     MEDLINE=99246375; PubMed=10229568;
RX
     Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
RA
RA
     Miyata T.;
RT
     "Extensive gene duplication in the early evolution of animals before
RT
     the parazoan-eumetazoan split demonstrated by G proteins and protein
RT
     tyrosine kinases from sponge and hydra.";
RL
     J. Mol. Evol. 48:646-653(1999).
RN
     [2]
RP
     SEQUENCE FROM N.A.
RX
     MEDLINE=21601119; PubMed=11738833;
RA
     Suga H., Katoh K., Miyata T.;
RT
     "Sponge homologs of vertebrate protein tyrosine kinases and frequent
RT
     domain shufflings in the early evolution of animals before the
RT
     parazoan-eumetazoan split.";
RL
     Gene 280:195-201(2001).
DR
     EMBL; AB006570; BAA81724.2; -.
DR
     HSSP; P08631; 1AD5.
DR
     GO; GO:0016020; C:membrane; IEA.
DR
     GO; GO:0005524; F:ATP binding; IEA.
     GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
     GO; GO:0004872; F:receptor activity; IEA.
     GO; GO:0016740; F:transferase activity; IEA.
DR
     GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR
DR
     GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR
     InterPro; IPR000494; EGFR L domain.
DR
     InterPro; IPR006211; Furin-like.
DR
     InterPro; IPR006212; Furin repeat.
     InterPro; IPR009030; Grow_fac_recep.
     InterPro; IPR000719; Prot kinase.
DR
DR
     InterPro; IPR001368; TNFR c6.
     InterPro; IPR001245; Tyr pkinase.
DR
     InterPro; IPR008266; Tyr_pkinase_AS.
DR
DR
     Pfam; PF00757; Furin-like; 1.
DR
     Pfam; PF00069; pkinase; 1.
     Pfam; PF01030; Recep L domain; 2.
     PRINTS; PR00109; TYRKINASE.
DR
     ProDom; PD000001; Prot kinase; 1.
DR
     SMART; SM00261; FU; 6.
DR
     SMART; SM00219; TyrKc; 1.
DR
     PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR
    PROSITE; PS50011; PROTEIN KINASE DOM; 1.
    PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR
    PROSITE; PS00652; TNFR NGFR 1; 1.
KW
    ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
     SEQUENCE 1193 AA; 128169 MW; 009E4AC9BC12DF60 CRC64;
SQ
  Query Match
                           8.9%; Score 85.5; DB 5; Length 1193;
                         22.3%; Pred. No. 7.8;
  Best Local Similarity
           37; Conservative 28; Mismatches
                                                 56; Indels
                                                                45; Gaps
           2 LQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPP-----LTCQRYCNASVTNSVKGTNAIL 56
Qу
              | ::| : || |: |: || : |
                                                  : | |: : |:
Db
         715 LCVSGCSNDTEYQDAALN-CLPCAAGCIGCSGPSISQCLTCA--SGSCTTTDVQSSGGII 771
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QУ
           57 WTCLGLSLIISLA---VFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEI 113
                  | ::| | | : | : |: ::| : :|
Db
          772 GIVFGSIVVIFLATSIVLILFIVYRRYEHKVFKNRTQSTA---MCYSN-----GNET 820
          114 ILPRGLEYTVEECTCEDCIKSKPKVDSDH----CFPLPAMEEGATI 155
Qу
                  ||: | | |:|:| :
          821 LRP-----PKLPPDATRLIITPETALEQGQVL 847
Db
RESULT 11
Q8RWV7
ID
     Q8RWV7
                PRELIMINARY:
                                  PRT:
                                         938 AA.
AC
     08RWV7;
DT
     01-JUN-2002 (TrEMBLrel. 21, Created)
DT
     01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT
     01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
     Hypothetical protein.
GN
     AT3G48195.
OS
     Arabidopsis thaliana (Mouse-ear cress).
OC
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC
     eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX
     NCBI TaxID=3702;
RN
     [1]
RP
     SEQUENCE FROM N.A.
RA
     Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA
     Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA
     Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA
     Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
     Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA
     Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA
     Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA
     Davis R.W., Ecker J.R., Theologis A.;
RT
     "Arabidopsis Full Length cDNA Clones.";
RL
     Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR
     EMBL; AY091078; AAM13898.1; -.
DR
     GO; GO:0016020; C:membrane; IEA.
     GO; GO:0005489; F:electron transporter activity; IEA.
DR
     GO; GO:0006118; P:electron transport; IEA.
     GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR
DR
     GO; GO:0006810; P:transport; IEA.
DR
     InterPro; IPR000515; BPD transp.
DR
    InterPro; IPR000345; CytC heme BS.
DR
    InterPro; IPR001683; PX.
DR
    Pfam; PF00787; PX; 1.
DR
    SMART; SM00312; PX; 1.
    PROSITE; PS00402; BPD TRANSP INN MEMBR; 1.
DR
DR
    PROSITE; PS00190; CYTOCHROME C; 2.
    PROSITE; PS50195; PX; 1.
DR
KW
    Hypothetical protein.
SQ
    SEQUENCE 938 AA; 103602 MW; 3E78395D65D75C95 CRC64;
 Query Match
                          8.7%; Score 83.5; DB 10; Length 938;
 Best Local Similarity 29.4%; Pred. No. 9.6;
 Matches 37; Conservative 18; Mismatches 28; Indels 43; Gaps
                                                                           9;
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QУ
           38 QRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD-EFKN--TGS 94
                     |: | :| ||:|
           29 ERYCSA---NSALGTPSM---C------STGPFQDSEFENFSLGP 62
Db
Qу
          95 GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP----KVDSDHCFPLPAM 149
              63 SLVKLSSLDM--SRLGD----RGIHFFDEGGSCNGRSSSAPGLNTGNVNIDMCGDL--M 113
Db
Qу
         150 EEGATI 155
             : 1111
Db
         114 DGGATI 119
RESULT 12
Q9STR8
ID
    Q9STR8
              PRELIMINARY;
                               PRT: 1998 AA.
AC
     O9STR8;
DΤ
     01-MAY-2000 (TrEMBLrel. 13, Created)
DT
     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT
     01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DΕ
    Hypothetical protein.
GN
    T24C20 80.
OS
    Arabidopsis thaliana (Mouse-ear cress).
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
OC
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC
     eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX
    NCBI TaxID=3702;
RN
     [1]
RP
    SEQUENCE FROM N.A.
RA
    Choisne N., Robert C., Brottier P., Wincker P., Cattolico L.,
    Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd S.,
RA
RA
    Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL
    Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN
     [2]
RP
    SEQUENCE FROM N.A.
RA
    EU Arabidopsis sequencing project;
RL
    Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AL096856; CAB51067.1; -.
DR
    PIR; T13009; T13009.
DR
    GO; GO:0016020; C:membrane; IEA.
DR
    GO; GO:0005215; F:transporter activity; IEA.
DR
    GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR
    GO; GO:0006810; P:transport; IEA.
DR
    InterPro; IPR000515; BPD transp.
DR
   InterPro; IPR001683; PX.
   Pfam; PF00787; PX; 1.
DR
DR
   SMART; SM00312; PX; 1.
    PROSITE; PS00402; BPD TRANSP INN MEMBR; 1.
DR
    PROSITE; PS50195; PX; 1.
DR
KW
    Hypothetical protein.
SO
    SEQUENCE 1998 AA; 223513 MW; 8B3D6A03CD248F55 CRC64;
 Query Match
                         8.7%; Score 83.5; DB 10; Length 1998;
 Best Local Similarity 29.4%; Pred. No. 23;
 Matches 37; Conservative 18; Mismatches 28; Indels
                                                            43; Gaps
                                                                         9;
Qу
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:|||:|
                                                  1: | :| ||:| |
Db
        1089 ERYCSA---NSALGTPSM---C-----SSTGPFODSEFENFSLGP 1122
Qу
          95 GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP----KVDSDHCFPLPAM 149
             Db
        1123 SLVKLSSLDM--SRLGD----RGIHFFDEGGSCNGRSSSAPGLNTGNVNIDMCGDL--M 1173
        150 EEGATI 155
Qу
            : | | | |
Db
        1174 DGGATI 1179
RESULT 13
08C6R5
ID
             PRELIMINARY; PRT; 449 AA.
    Q8C6R5
AC
    Q8C6R5;
DT
    01-MAR-2003 (TrEMBLrel. 23, Created)
DT
    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
    Protein tyrosine kinase 2 beta (Fragment).
GN
    PTK2B.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=C57BL/6J; TISSUE=Oviduct;
RX
    MEDLINE=22354683; PubMed=12466851;
RA
    The FANTOM Consortium,
RA
    the RIKEN Genome Exploration Research Group Phase I & II Team;
    "Analysis of the mouse transcriptome based on functional annotation of
RТ
RT
    60,770 full-length cDNAs.";
RL
    Nature 420:563-573(2002).
DR
    EMBL; AK054002; BAC35615.1; -.
    MGD; MGI:104908; Ptk2b.
DR
DR
    GO; GO:0005515; F:protein binding; IPI.
DR
    GO; GO:0004672; F:protein kinase activity; IDA.
    GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
    InterPro; IPR000299; Band 4.1.
DR
    SMART; SM00295; B41; 1.
    PROSITE; PS50057; FERM 3; 1.
DR
FT
    NON TER 449
                   449
SO
    SEQUENCE
              449 AA; 51577 MW; D3565BCBA7D32B84 CRC64;
 Query Match
                       8.6%; Score 83; DB 11; Length 449;
 Best Local Similarity 26.9%; Pred. No. 4.6;
 Matches 29; Conservative 13; Mismatches
                                            34; Indels
                                                       32; Gaps
         88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
Qу
            Db
        249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSODTKPTCLAEFKQI 305
        139 DSDHCFPLPAME-----EGATILVTTKTND-----YCK 166
QУ
             306 KSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR 353
Db
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RESULT 14
08C9L4
ID
     Q8C9L4
                 PRELIMINARY;
                                  PRT;
                                          474 AA.
AC
     Q8C9L4;
DТ
     01-MAR-2003 (TrEMBLrel. 23, Created)
     01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DΤ
DT
     01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
     Protein tyrosine kinase 2 beta.
GN
     PTK2B.
OS
     Mus musculus (Mouse).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
     NCBI TaxID=10090;
RN
     [1]
RP
     SEQUENCE FROM N.A.
     STRAIN=C57BL/6J; TISSUE=Thymus;
RC
RX
     MEDLINE=22354683; PubMed=12466851;
RA
     The FANTOM Consortium,
RA
     the RIKEN Genome Exploration Research Group Phase I & II Team;
RT
     "Analysis of the mouse transcriptome based on functional annotation of
RТ
     60,770 full-length cDNAs.";
RL
     Nature 420:563-573(2002).
DR
     EMBL; AK041878; BAC31090.1; -.
DR
     MGD; MGI:104908; Ptk2b.
DR
     GO; GO:0005515; F:protein binding; IPI.
     GO; GO:0004672; F:protein kinase activity; IDA.
DR
DR
     GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR
     InterPro; IPR000299; Band 4.1.
DR
     SMART; SM00295; B41; 1.
DR
     PROSITE; PS50057; FERM 3; 1.
SO
     SEOUENCE
               474 AA; 54201 MW; A1A83BCB191B55FB CRC64;
  Query Match
                          8.6%; Score 83; DB 11; Length 474;
  Best Local Similarity
                         26.9%; Pred. No. 4.9;
          29; Conservative 13; Mismatches 34; Indels
                                                               32; Gaps
                                                                            4:
           88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
Qу
                     | | :| |:|:
                                                         : |
                                                                |:
          249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDTKPTCLAEFKQI 305
         139 DSDHCFPLPAME-----EGATILVTTKTND------YCK 166
Qу
                       :
                                | | | | :: | | ::
Db
         306 KSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR 353
RESULT 15
097491
ID
    097491
                PRELIMINARY:
                                 PRT; 327 AA.
    097491;
АC
    01-MAY-1999 (TrEMBLrel. 10, Created)
    01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
    Fas protein.
GN
    FAS.
OS
    Ovis aries (Sheep).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
    Bovidae; Caprinae; Ovis.
OX
    NCBI TaxID=9940;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RÇ
    TISSUE=Lymphocytes;
RA
    Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RT
    "Cloning of sheep fas antigen.";
    Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AB011671; BAA37093.1; -.
    HSSP; P25445; 1DDF.
DR
DR
    GO; GO:0016020; C:membrane; IEA.
    GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR
DR
    GO; GO:0006915; P:apoptosis; IEA.
DR
    GO; GO:0006955; P:immune response; IEA.
DR
    GO; GO:0007165; P:signal transduction; IEA.
DR
    InterPro; IPR000488; Death.
DR
    InterPro; IPR008063; Fas receptor.
DR
    InterPro; IPR001368; TNFR c6.
DR
    Pfam; PF00531; death; 1.
DR
    Pfam; PF00020; TNFR c6; 3.
    PRINTS; PR01680; FASRECEPTOR.
DR
    SMART; SM00005; DEATH; 1.
    SMART; SM00208; TNFR; 3.
    PROSITE; PS50017; DEATH DOMAIN; 1.
DR
    PROSITE; PS50050; TNFR NGFR 2; 2.
DR
SO
    SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE387A CRC64;
 Query Match
                      8.5%; Score 82; DB 6; Length 327;
 Best Local Similarity 23.0%; Pred. No. 4;
 Matches 54; Conservative 25; Mismatches 68; Indels 88; Gaps
Qу
          8 CSQ-NEYFDSLLHA--CIPCQL----T 32
            \Box
Db
         84 CSEGNEYTDKSHHSDKCIRCSVCDEEHGLEVEHNCTRTQNTKCRCKSNFFCNSSPCEHCN 143
         33 PPLTCQ----RYCNASVTNSVKG----TNAILWTCLGLSLIISLAVFVLMFLLRK---- 79
Qу
           Db
        144 PCTTCEHGIIEKCTPTSNTKCKGSRSHTNS-LWALLILLLLILIFLIIYKVVRRRRRNKK 202
         80 ---ISSEPLKDEFKNTGSGLLGMANIDLEKSRTG-----DEIILPRGLEYTVEEC 126
QУ
               Db
        203 NGNCVSAASSDEGRQ----LNLTDVDLGKYIPSIAELMKITEVKEFVRKNGM---EEA 253
        127 TCEDCIKSKPKVDSDHCFPLPAMEEGATIL----VTTKTNDYC---KSLPAALS 173
QУ
             Db
        254 KIDDIMH-----DNLH----ETAEQKVQLLRKWYQSHGKKNAYCTLTKNLPKALA 299
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Search completed: April 19, 2004, 13:22:55 Job time: 29.2593 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2004, 13:17:02; Search time 7.57202 Seconds

(without alignments)

1265.305 Million cell updates/sec

Title: PCT-US03-05147-1

Perfect score: 964

Sequence: 1 MLQMAGQCSQNEYFDSLLHA.....CKSLPAALSATEIEKSISAR 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt 42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		용				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	964	100.0	184	 1	TR17 HUMAN	Q02223 homo sapien
2	572	59.3	185	1	TR17 MOUSE	088472 mus musculu
3	116.5	12.1	175	1	T13C MOUSE	Q9d8d0 mus musculu
4	94	9.8	323	1	TNR6 BOVIN	P51867 bos taurus
5	93	9.6	184	1	T13C HUMAN	Q96rj3 homo sapien
6	86.5	9.0	867	1	PML1 MOUSE	054990 mus musculu
7	82	8.5	1009	1	FAK2 MOUSE	Q9qvp9 m protein t
8	82	8.5	1009	1	FAK2 RAT	P70600 rattus norv
9	79.5	8.2	1009	1	FAK2 HUMAN	Q14289 h protein t
10	78.5	8.1	293	1	T13X HUMAN	014836 homo sapien
11	78.5	8.1	343	1	MJK2 METJA	Q58752 methanococc
12	77	8.0	249	1	T13X MOUSE	Q9et35 mus musculu
13	76	7.9	748	1	CI84 NEUCR	042637 neurospora
14	75.5	7.8	638	1	YCSB SCHPO	074910 schizosacch
15	75	7.8	849	1	SRK6 BRAOL	Q09092 brassica ol
16	74.5	7.7	384	1	ERD1 KLULA	P41771 kluyveromyc
17	72.5	7.5	1013	1	PRML DROME	P82295 drosophila

18	71.5	7.4	105	1	Y078_NPVOP	010331 orgyia pseu
19	71.5	7.4	330	1	OR08_MOUSE	Q8vf13 mus musculu
20	71.5	7.4	627	1	Y017 RICPR	Q9zec6 rickettsia
21	71	7.4	227	1	COMB_THEMA	Q9wzq4 thermotoga
22	71	7.4	314	1	OR11 MOUSE	Q8vgr9 mus musculu
23	70.5	7.3	154	1	CYY1 HUMAN	Q96j86 homo sapien
24	70.5	7.3	188	1	Y101_UREPA	Q9pr43 ureaplasma
25	70.5	7.3	1203	1	MGR5_RAT	P31424 rattus norv
26	70.5	7.3	1877	1	PCK5 MOUSE	Q04592 mus musculu
27	70.5	7.3	2715	1	G156 PARPR	P13837 paramecium
28	70	7.3	654	1	HS70_TRIRU	093866 trichophyto
29	69.5	7.2	573	1	TLPC_BACSU	P39209 bacillus su
30	69.5	7.2	1212	1	MGR5_HUMAN	P41594 homo sapien
31	69.5	7.2	5376	1	ZAN_MOUSE	088799 mus musculu
32	69	7.2	324	1	GC1 MOUSE	P01868 mus musculu
33	69	7.2	352	1	C5AR_RAT	P97520 rattus norv
34	69	7.2	379	1	PANE_YEAST	P38787 saccharomyc
35	69	7.2	393	1	GC1M_MOUSE	P01869 mus musculu
36	69	7.2	416	1	R23B_MOUSE	P54728 mus musculu
37	69	7.2	704	1	MID2_SCHPO	Q9p7y8 schizosacch
38	69	7.2	791	1	SYFB_XANCP	Q8p7z6 xanthomonas
39	69	7.2	943	1	UVRA_STRMU	P72481 streptococc
40	68.5	7.1	213	1	RL1_METMA	Q8py52 methanosarc
41	68.5	7.1	321	1	O5V1_HUMAN	Q9ugf6 homo sapien
42	68.5	7.1	328	1	Y679_CHLMU	Q9pjz7 chlamydia m
43	68.5	7.1	409	1	R23B_HUMAN	P54727 homo sapien
44	68.5	7.1	575	1	CH62_CUCMA	Q05046 cucurbita m
45	68.5	7.1	576	1	CH62_MAIZE	Q43298 zea mays (m

ALIGNMENTS

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RESULT 1
TR17_HUMAN
ID
     TR17 HUMAN
                    STANDARD;
                                    PRT;
                                           184 AA.
AC
     002223;
DT
     01-JUL-1993 (Rel. 26, Created)
DT
     01-JUL-1993 (Rel. 26, Last sequence update)
DT
     10-OCT-2003 (Rel. 42, Last annotation update)
DΕ
     Tumor necrosis factor receptor superfamily member 17 (B-cell
DE
     maturation protein).
GN
     TNFRSF17 OR BCMA OR BCM.
OS
     Homo sapiens (Human).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX
     NCBI_TaxID=9606;
RN
     [1]
RΡ
     SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
RC
     TISSUE=Lymph node, and Peripheral blood leukocytes;
RX
     MEDLINE=93010984; PubMed=1396583;
RA
     Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
RA
     Larsen C.J., Tsapis A.;
     "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
RT
     by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";
RΤ
RL
     EMBO J. 11:3897-3904(1992).
RN
     [2]
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RP
     SEQUENCE FROM N.A.
RX
     MEDLINE=94218235; PubMed=8165126;
RA
     Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
RT
     "The BCMA gene, preferentially expressed during B lymphoid
RT
     maturation, is bidirectionally transcribed.";
RL
     Nucleic Acids Res. 22:1147-1154(1994).
RN
RP
     SEQUENCE FROM N.A.
RX
     MEDLINE=99425270; PubMed=10493829;
RA
     Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
     Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
RA
RA
     Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
RA
     Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT
     "Genome duplications and other features in 12 Mb of DNA sequence from
RT
     human chromosome 16p and 16q.";
RL
     Genomics 60:295-308(1999).
RN
     SEQUENCE FROM N.A., AND VARIANT THR-153.
RP
RX
    MEDLINE=21419161; PubMed=11528522;
     Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;
RA
RT
     "Presence of four major haplotypes in human BCMA gene: lack of
RT
     association with systemic lupus erythematosus and rheumatoid
RT
     arthritis.";
RL
     Genes Immun. 2:276-279(2001).
RN
     FUNCTION, AND INTERACTION WITH TRAF1 AND TRAF3.
RΡ
RX
     MEDLINE=20363816; PubMed=10903733;
RA
     Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,
RA
     Inoue J.-I., Devergne O., Tsapis A.;
RT
     "TNF receptor family member BCMA (B cell maturation) associates with
     TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and
RT
     activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38
RT
RΤ
    mitogen-activated protein kinase.";
RL
    J. Immunol. 165:1322-1330(2000).
RN
    FUNCTION.
RP
RX
    MEDLINE=20259066; PubMed=10801128;
RA
    Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
RA
    Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
RA
    Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
RA
     Harrison K., Kindsvogel W., Clegg C.H.;
     "TACI and BCMA are receptors for a TNF homologue implicated in B-cell
RТ
RТ
    autoimmune disease.";
    Nature 404:995-999(2000).
RL
RN
RP
    FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
    MEDLINE=21170294; PubMed=10973284;
RX
RA
    Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA
    McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA
     Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT
     "APRIL and TALL-I and receptors BCMA and TACI: system for regulating
RT
    humoral immunity.";
RL
    Nat. Immunol. 1:252-256(2000).
RN
RP
    INTERACTION WITH TRAF5 AND TRAF6.
RX
    MEDLINE=20381353; PubMed=10908663;
RA
    Shu H.-B., Johnson H.;
```

```
RΤ
     "B cell maturation protein is a receptor for the tumor necrosis factor
RТ
     family member TALL-1.";
RL
    Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
    -!- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
CC
        Promotes B-cell survival and plays a role in the regulation of
CC
        humoral immunity. Activates NF-kappa-B and JNK.
CC
    -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC
CC
    -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
CC
        and perinuclear Golgi-like structures.
    -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
CC
CC
        cells or monocytes.
    -!- DISEASE: A form of T-cell acute lymphoblastic leukemia (T-ALL) is
CC
        characterized by a chromosomal translocation t(4;16)(q26;p13)
CC
CC
        which involves BCMA and IL2.
    -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
    _____
CC
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    between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC
    EMBL; Z14954; CAA78679.1; -.
DR
    EMBL; Z29575; CAA82691.1; -.
DR
    EMBL; Z29574; CAA82690.1; -.
DR
    EMBL; U95742; AAB67251.1; -.
DR
    EMBL; AB052772; BAB60895.1; -.
DR
    PIR; S43486; S43486.
DR
    Genew; HGNC:11913; TNFRSF17.
DR
DR
    MIM; 109545; -.
    GO; GO:0016021; C:integral to membrane; TAS.
DR
DR
    GO; GO:0005886; C:plasma membrane; TAS.
    GO; GO:0004872; F:receptor activity; TAS.
DR
    GO; GO:0008283; P:cell proliferation; TAS.
DR
    GO; GO:0007275; P:development; TAS.
DR
    GO; GO:0007165; P:signal transduction; TAS.
DR
    Receptor; Immune response; Proto-oncogene; Signal-anchor;
KW
    Transmembrane; Chromosomal translocation; Polymorphism.
KW
                       54
                                 EXTRACELLULAR (POTENTIAL).
FT
    DOMAIN
                 1
                                SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
    TRANSMEM
                 55
                        77
FT
                                (POTENTIAL).
\operatorname{FT}
                 78 184
FT
    DOMAIN
                                CYTOPLASMIC (POTENTIAL).
FT
    REPEAT
                 7
                      41
                                TNFR-CYS.
                 3
                                BREAKPOINT FOR TRANSLOCATION TO FORM
FT
                        4
    SITE
                                 INTERLEUKIN 2/BCM ONCOGENE.
FT
                 8
FT
                        21
                                BY SIMILARITY.
    DISULFID
                       37
                                BY SIMILARITY.
FT
    DISULFID
                 24
                       41
FT
    DISULFID
                28
                                BY SIMILARITY.
               153 153
FT
    VARIANT
                                A \rightarrow T.
\Gamma T
                                 /FTId=VAR 012234.
     SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;
SO
  Query Match
                         100.0%; Score 964; DB 1; Length 184;
  Best Local Similarity 100.0%; Pred. No. 6.8e-83;
                                                                           0;
  Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps
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Qу
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Qу
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Db
         121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEJEKS 180
Qу
             Db
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         181 ISAR 184
Qу
             Db
         181 ISAR 184
RESULT 2
TR17 MOUSE
    TR17 MOUSE
ID
                  STANDARD;
                                 PRT;
                                       185 AA.
    088472;
AC
    28-FEB-2003 (Rel. 41, Created)
DT
    28-FEB-2003 (Rel. 41, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
    Tumor necrosis factor receptor superfamily member 17 (B-cell
DE
DE
    maturation protein).
GN
    TNFRSF17 OR BCMA OR BCM.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
OX
    NCBI TaxID=10090;
RN
    [1]
RP
    SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
    STRAIN=BALB/c; TISSUE=Spleen;
RC
RX
    MEDLINE=99061155; PubMed=9846698;
    Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
RA
    Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
RA
    "The characterization of murine BCMA gene defines it as a new member
RT
    of the tumor necrosis factor receptor superfamily.";
RT
    Int. Immunol. 10:1693-1702(1998).
RL
RN
    [2]
    SEQUENCE FROM N.A. (ISOFORM 1).
RP
    STRAIN=C57BL/6J; TISSUE=Colon;
RC
RX
    MEDLINE=21085660; PubMed=11217851;
RA
    Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
    Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA
    Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA
RA
    Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA
    Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
    Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA
    Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA
RA
    Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA
    Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA
    Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA
    Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA
    Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
```

```
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA
    Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA
    Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA
    Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA
RA
    Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA
    Hayashizaki Y.;
RT
    "Functional annotation of a full-length mouse cDNA collection.";
    Nature 409:685-690(2001).
RL
CC
    -!- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
CC
        Promotes B-cell survival and plays a role in the regulation of
CC
        humoral immunity. Activates NF-kappa-B and JNK (By similarity).
    -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
CC
CC
        similarity).
    -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC
CC
    -!- ALTERNATIVE PRODUCTS:
CC
        Event=Alternative splicing; Named isoforms=2;
CC
        Name=1;
          IsoId=088472-1; Sequence=Displayed;
CC
CC
        Name=2;
          IsoId=088472-2; Sequence=VSP 006507;
CC
    -!- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
CC
CC
        heart, and at lower levels in kidney and lung.
CC
    -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
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    or send an email to license@isb-sib.ch).
CC
CC
    _____
    EMBL; AF061505; AAC23799.1; -.
DR
DR
    EMBL; AK020247; BAB32038.1; -.
DR
    MGD; MGI:1343050; Tnfrsf17.
KW
    Receptor; Immune response; Signal-anchor; Transmembrane;
    Alternative splicing.
KW
    DOMAIN
                1
                       49
                               EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
                 50
                       70
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FT
                               (TYPE III MEMBRANE PROTEIN) (POTENTIAL).
FT
                    185
                 71
FT
    DOMAIN
                               CYTOPLASMIC (POTENTIAL).
                     36
                               TNFR-CYS.
FT
    REPEAT
                 4
                      18
                 5
                               BY SIMILARITY.
FT
    DISULFID
                      32
                21
                               BY SIMILARITY.
FT
    DISULFID
                 25
                      36
                               BY SIMILARITY.
FT
    DISULFID
FT
    VARSPLIC
               87
                      91
                               Missing (in isoform 2).
                               /FTId=VSP 006507.
FT
    SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;
SQ
                        59.3%; Score 572; DB 1; Length 185;
  Query Match
  Best Local Similarity 62.6%; Pred. No. 2.5e-46;
  Matches 117; Conservative 21; Mismatches 41; Indels
           4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
QУ
             1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58
Db
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64 LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
QУ
             1::|||:| : |||||:: | ||||| ::
                                             59 LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL 118
Db
QУ
         120 EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
              119 EYTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALOSVMGM 178
Db
         178 EKSISAR 184
Qy
             - 1
         179 EKPTHTR 185
Db
RESULT 3
T13C MOUSE
     T13C MOUSE
                   STANDARD;
                                  PRT:
                                         175 AA.
AC
     09D8D0:
DT
     28-FEB-2003 (Rel. 41, Created)
     28-FEB-2003 (Rel. 41, Last sequence update)
DT
     28-FEB-2003 (Rel. 41, Last annotation update)
DT
    Tumor necrosis factor receptor superfamily member 13C (B cell-
DE
     activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor
DE
DE
     3) (B-cell maturation defect).
    TNFRSF13C OR BAFFR OR BCMD OR BR3.
GN
    Mus musculus (Mouse).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
OX
    NCBI TaxID=10090;
    [1]
RN
     SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP
     STRAIN=BALB/c; TISSUE=B-cell lymphoma;
RC
RX
    MEDLINE=21442025; PubMed=11509692;
    Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA
     Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA
     Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
RA
    Ambrose C.;
RA
RT
    "BAFF-R, a newly identified TNF receptor that specifically interacts
     with BAFF.";
RT
RL
     Science 293:2108-2111(2001).
RN
     SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
RP
RC
     STRAIN=A/J;
    MEDLINE=21475520; PubMed=11591325;
RX
    Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
RA
     Cancro M.P., Grewal I.S., Dixit V.M.;
     "Identification of a novel receptor for B lymphocyte stimulator that
RT
     is mutated in a mouse strain with severe B cell deficiency.";
RT
     Curr. Biol. 11:1547-1552(2001).
RL
RN
     [3]
RP
     SEQUENCE FROM N.A. (ISOFORM 1).
     STRAIN=C57BL/6J; TISSUE=Small intestine;
RC
RX
    MEDLINE=21085660; PubMed=11217851;
     Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA
    Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA
     Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA
     Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA
     Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA
```

```
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA
RA
     Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
     Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA
     Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA
     Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA
RA
     Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA
     Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
     Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA
     Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA
     Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA
     Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA
     Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA
RA
     Hayashizaki Y.;
     "Functional annotation of a full-length mouse cDNA collection.";
RT
RL
     Nature 409:685-690(2001).
RN
     [4]
RP
    FUNCTION.
    MEDLINE=21614654; PubMed=11747827;
RX
     Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,
RA
RA
     Hilbert D.M., Hayes C.E., Cancro M.P.;
RT
     "Competition for BLyS-mediated signaling through Bcmd/BR3 regulates
RT
    peripheral B lymphocyte numbers.";
    Curr. Biol. 11:1986-1989(2001).
RL
     -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLyS.
CC
         Promotes the survival of mature B-cells and the B-cell response.
CC
CC
    -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC
     -!- ALTERNATIVE PRODUCTS:
         Event=Alternative splicing; Named isoforms=2;
CC
CC
CC
           IsoId=Q9D8D0-1; Sequence=Displayed;
CC
         Name=2;
           IsoId=Q9D8D0-2; Sequence=VSP 006506;
CC
    -!- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
CC
CC
        detected at lower levels in lung and thymus.
CC
    -!- DISEASE: Defects in TNFRSF13C are a cause of severe B-cell
         deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion
CC
         in the BAFFR gene leading to an altered C-terminus. The mutant RNA
CC
         is not detectable. B-cell lymphopoiesis is normal, but the life
CC
CC
         span of peripheral B-cells is much reduced.
     -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
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CC
     or send an email to license@isb-sib.ch).
CC
     EMBL; AF373847; AAK91827.1; -.
DR
DR
     EMBL; AK008142; BAB25490.1; -.
     MGD; MGI:1919299; Tnfrsf13c.
ΚW
     Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW
     Alternative splicing.
FT
                         71
                                  EXTRACELLULAR (POTENTIAL).
     DOMAIN
                  1
FT
     TRANSMEM
                  72
                         92
                                  SIGNAL-ANCHOR
FT
                                  (TYPE III MEMBRANE PROTEIN) (POTENTIAL).
```

```
175
                               CYTOPLASMIC (POTENTIAL).
FT
    DOMAIN
                93
                21
                      38
                               TNFR-CYS (PARTIAL).
FT
    REPEAT
               22
                      35
                               BY SIMILARITY.
FT
    DISULFID
                      38
                                BY SIMILARITY.
FT
    DISULFID
                27
                                N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
    CARBOHYD
                23
                       23
FT
    VARSPLIC
               133
                      143
                               Missing (in isoform 2).
                               /FTId=VSP 006506.
FT
    SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;
SQ
                        12.1%; Score 116.5; DB 1; Length 175;
 Query Match
 Best Local Similarity 29.4%; Pred. No. 0.00074;
         50; Conservative 21; Mismatches 64; Indels
                                                          35; Gaps
                                                                        8;
           7 QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
Qу
                                       21 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80
          57 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111
Qу
                | |:|: :|| : || | | || ::|
                                                        : |: : | |
          81 GLILALTLVGLVSLVSWRWRQQLRTASPDTSEGVQQE-----SLENVFVPSSET-- 129
Db
         112 EIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT 161
QУ
                130 ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSTELVTTKT 170
Db
RESULT 4
TNR6 BOVIN
    TNR6 BOVIN
                                PRT: 323 AA.
                  STANDARD;
    P51867;
    01-OCT-1996 (Rel. 34, Created)
DТ
    01-OCT-1996 (Rel. 34, Last sequence update)
DT
    28-FEB-2003 (Rel. 41, Last annotation update)
DT
    Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE
    receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE
DE
    (CD95).
    TNFRSF6 OR APT1 OR FAS.
GN
    Bos taurus (Bovine).
OS
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC
OC
    Bovidae; Bovinae; Bos.
    NCBI TaxID=9913;
OX
RN
    [1]
    SEQUENCE FROM N.A.
RP
    MEDLINE=96226401; PubMed=8634151;
RX
    Yoo J., Stone R.T., Beattie C.W.;
RA
    "Cloning and characterization of the bovine Fas.";
RT
    DNA Cell Biol. 15:227-234(1996).
RL
    -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC
        recruits caspase-8 to the activated receptor. The resulting death-
CC
        inducing signaling complex (DISC) performs caspase-8 proteolytic
CC
        activation which initiates the subsequent cascade of caspases
CC
        (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC
        mediated apoptosis may have a role in the induction of peripheral
CC
CC
        tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC
        both (By similarity).
    -!- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC
```

```
-!- SUBCELLULAR LOCATION: Type I membrane protein.
CC
     -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
         AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC
     -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC
CC
     -!- SIMILARITY: Contains 1 death domain.
     _____
CC
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     or send an email to license@isb-sib.ch).
CC
     CC
DR
     EMBL; U34794; AAC48546.1; -.
     HSSP; P25445; 1DDF.
     InterPro; IPR000488; Death.
DR
     InterPro; IPR008063; Fas receptor.
DR
     InterPro; IPR001368; TNFR c6.
DR
     Pfam; PF00531; death; 1.
DR
     Pfam; PF00020; TNFR c6; 3.
DR
     PRINTS; PR01680; FASRECEPTOR.
DR
     SMART; SM00005; DEATH; 1.
     SMART; SM00208; TNFR; 3.
DR
     PROSITE; PS00652; TNFR NGFR 1; 2.
DR
     PROSITE; PS50050; TNFR NGFR 2; 2.
DR
     PROSITE; PS50017; DEATH DOMAIN; 1.
DR
     Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
KW
                                  POTENTIAL.
     SIGNAL 1 16
FT
                                    TUMOR NECROSIS FACTOR RECEPTOR
                   17
                         323
FT
     CHAIN
                                    SUPERFAMILY MEMBER 6.
FT

        DOMAIN
        17
        170

        TRANSMEM
        171
        188

        DOMAIN
        189
        323

                                    EXTRACELLULAR (POTENTIAL).
FT
                                    POTENTIAL.
FT
     TRANSMEM 171 188 POTENTIAL.

DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).

REPEAT 45 80 TNFR-CYS 1.

REPEAT 81 124 TNFR-CYS 2.

REPEAT 125 163 TNFR-CYS 3.

DOMAIN 238 306 DEATH.

DISULFID 45 56 BY SIMILARITY.

DISULFID 57 70 BY SIMILARITY.

DISULFID 60 79 BY SIMILARITY.

DISULFID 82 98 BY SIMILARITY.

DISULFID 101 116 BY SIMILARITY.

DISULFID 101 116 BY SIMILARITY.

DISULFID 104 124 BY SIMILARITY.
FT
FΤ
FT
FT
FT
FT
FT
     DISULFID 60 79
DISULFID 82 98
DISULFID 101 116
FT
FT
FT
                                    BY SIMILARITY.
     DISULFID 104 124
FT
     DISULFID 126 140
                                    BY SIMILARITY.
     DISULFID 143 154
FT
                                    BY SIMILARITY.
    DISULFID 146 162 BY SIMILARITY.

CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT
FT
FT
     SEQUENCE 323 AA; 36445 MW; 4D88A90E9E1F4892 CRC64;
SO
  Ouery Match
                             9.8%; Score 94; DB 1; Length 323;
  Best Local Similarity 22.1%; Pred. No. 0.18;
  Matches 51; Conservative 33; Mismatches 65; Indels 82; Gaps 15;
             8 CSQ-NEYFDSLLHA--CIPCQL----T 32
Qу
```

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82 CSEGNEYTDKSHHSDKCIRCSICDEEHGLEVEQNCTRTRNTKCRCKSNFFCNSSPCEHCN 141
Db
          33 PPLTCQ----RYCNASVTNSVKGTNA---ILWTCLGLSLIISLAVFVLMFLLRKISSEPL 85
Qу
                                  ||::
                                                  | | | : : : : : : : |
             | ||:
                        1:
                                         | | |
          142 PCTTCEHGIIEKCTPTSNTKCKGSRSHANSLWAL----LILLIPIVLIIYKVVKSRERNK 197
Db
          86 KDEFKNTGSG----LLGMANIDL-----EKSRTGD--EIILPRGLEYTVEECTCED 130
QУ
             |:|:|:
                                                                - 11
          198 KNDYCNSAASNDEGRQLNLTDVDLGKYIPSIAEQMRITEVKEFVRKNGM----EEAKIDD 253
Db
         131 CIKSKPKVDSDHCFPLPAMEEGATILVT----TKTNDYC---KSLPAALS 173
QУ
                  |: | |: :|
                                                      254 IMH----DNVH----ETAEQKVQLLRNWYQSHGKKNAYCTLTKSLPKALA 295
Db
RESULT 5
T13C HUMAN
    T13C HUMAN
                                  PRT; 184 AA.
                   STANDARD;
AC
     Q96RJ3;
     28-FEB-2003 (Rel. 41, Created)
DT
    28-FEB-2003 (Rel. 41, Last sequence update)
DT
    10-OCT-2003 (Rel. 42, Last annotation update)
DT
    Tumor necrosis factor receptor superfamily member 13C (B cell-
    activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor
DE
DE
     3).
    TNFRSF13C OR BAFFR OR BR3.
GN
OS
    Homo sapiens (Human).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
OX
    NCBI TaxID=9606;
RN
    [1]
    SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP
    TISSUE=B-cell lymphoma;
RC
    MEDLINE=21442025; PubMed=11509692;
RX
    Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA
    Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA
     Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
RA
    Ambrose C.;
RA
     "BAFF-R, a newly identified TNF receptor that specifically interacts
RT
     with BAFF.";
RT
     Science 293:2108-2111(2001).
RL
RN
     [2]
    FUNCTION.
RP
    MEDLINE=21475520; PubMed=11591325;
RX
     Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
RA
     Cancro M.P., Grewal I.S., Dixit V.M.;
RA
     "Identification of a novel receptor for B lymphocyte stimulator that
RT
     is mutated in a mouse strain with severe B cell deficiency.";
RT
    Curr. Biol. 11:1547-1552(2001).
RL
CC
    -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLyS.
        Promotes the survival of mature B-cells and the B-cell response.
CC
CC
    -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC
    -!- ALTERNATIVE PRODUCTS:
CC
        Event=Alternative splicing; Named isoforms=2;
CC
        Name=1;
CC
           IsoId=Q96RJ3-1; Sequence=Displayed;
CC
        Name=2;
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IsoId=Q96RJ3-2; Sequence=VSP 006505;
CC
CC
         Note=No experimental confirmation available;
CC
    -!- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
CC
       in resting B-cells. Detected at lower levels in activated B-cells,
CC
       resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
CC
    -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
    _____
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    ______
    EMBL; AF373846; AAK91826.1; -.
DR
    PDB; 1MPV; 30-OCT-02.
DR
    Genew; HGNC:17755; TNFRSF13C.
DR
    MIM; 606269; -.
DR
    InterPro; IPR001368; TNFR c6.
DR
    PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR
    PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.
KW
    Receptor; Immune response; Signal-anchor; Transmembrane;
    Alternative splicing; 3D-structure.
FT
    DOMAIN
               1 78
                          EXTRACELLULAR (POTENTIAL).
FT
    TRANSMEM
               79
                    99
                            SIGNAL-ANCHOR
                           (TYPE III MEMBRANE PROTEIN) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
TNFR-CYS (PARTIAL).
FT
    DOMAIN 100 184
REPEAT 18 35
FT
FT
                    32
FT
   DISULFID
              19
                            BY SIMILARITY.
              24
                    35
FT
    DISULFID
                            BY SIMILARITY.
   VARSPLIC 143 143
                            P \rightarrow PA (in isoform 2).
                            /FTId=VSP 006505.
FT
    SEQUENCE 184 AA; 18863 MW; F2BFB98099A27138 CRC64;
SQ
                       9.6%; Score 93; DB 1; Length 184;
 Query Match
 Best Local Similarity 26.5%; Pred. No. 0.12;
 Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;
          8 CSONEYFDSLLHACIPCOL-----RCSSNTP--PLTCORYCNASVTNSVKGTNAIL 56
Qу
           19 CVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGLL 78
Db
         57 W---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEKS 107
Qу
                 Db
         79 FGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPL----- 127
        108 RTGDEIILPRGLEYTVEECTC-----EDCIKSKPKVDSDHCFPLPAMEEGATILVTTK 160
Qy
             128 --- DKVII---LSPGISDATAPAWPPPGEDPGTTPP----GHSVPVPATELGSTELVTTK 177
Db
        161 T 161
QУ
         1
        178 T 178
Db
```

```
PML1 MOUSE
                STANDARD; PRT; 867 AA.
ID
     PML1 MOUSE
     054990; 035408;
AC
     16-OCT-2001 (Rel. 40, Created)
DT
     16-OCT-2001 (Rel. 40, Last sequence update)
DT
     10-OCT-2003 (Rel. 42, Last annotation update)
DT
    Prominin 1 precursor (Prominin-like protein 1) (Antigen AC133
DE
DE
    homolog).
GN
    PROM1 OR PROML1 OR PROM.
OS
    Mus musculus (Mouse).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC
OX
    NCBI TaxID=10090;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
RC
    TISSUE=Brain;
    Miraglia S., Godfrey W., Buck D.;
RA
RL
    Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN
RP
    SEQUENCE FROM N.A.
RC
    TISSUE=Kidney;
RX
    MEDLINE=98024147; PubMed=9356465;
RA
    Weigmann A., Corbeil D., Hellwig A., Huttner W.B.;
RT
    "Prominin, a novel microvilli-specific polytopic membrane protein of
RT
     the apical surface of epithelial cells, is targeted to plasmalemmal
RT
    protrusions of non-epithelial cells.";
    Proc. Natl. Acad. Sci. U.S.A. 94:12425-12430(1997).
RL
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
    -!- TISSUE SPECIFICITY: In the embryo, expressed on the apical side of
CC
CC
        neuroepithelial cells and of other epithelia such as lung buds,
        gut and urether buds. In the adult, expressed at the apical side
CC
CC
        of the kidney tubules and of the ependymal layer of the brain. Not
CC
         expressed in gut, liver, lung, pituitary, adrenal, heart or
CC
        spleen.
CC
    -!- SIMILARITY: Belongs to the prominin family.
CC
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CC
     _____
    EMBL; AF039663; AAB96916.1; -.
DR
    EMBL; AF026269; AAB86715.1; -.
DR
    PIR; T08881; T08881.
DR
    MGD; MGI:1100886; Prom1.
DR
DR
    GO; GO:0005903; C:brush border; IDA.
    GO; GO:0005887; C:integral to plasma membrane; IDA.
DR
    GO; GO:0005902; C:microvillus; IDA.
DR
    InterPro; IPR008795; Prominin.
DR
    Pfam; PF05478; Prominin; 1.
    Signal; Transmembrane; Glycoprotein.
KW
                             POTENTIAL.
FT
    SIGNAL
            1 19
                                PROMININ 1.
FT
    CHAIN
                 20
                       867
FT
     DOMAIN
                 20
                       107
                                EXTRACELLULAR (POTENTIAL).
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TRANSMEM 108 128
DOMAIN 129 158
FT
                                               POTENTIAL.
FT
                                              CYTOPLASMIC (POTENTIAL).
FT
       TRANSMEM 159 179
                                             POTENTIAL.
     DOMAIN 180 434 EXTRACELLULAR (POTENTIAL).

TRANSMEM 435 455 POTENTIAL.

DOMAIN 456 487 CYTOPLASMIC (POTENTIAL).

TRANSMEM 488 508 POTENTIAL.

DOMAIN 509 794 EXTRACELLULAR (POTENTIAL).

TRANSMEM 795 815 POTENTIAL.

DOMAIN 816 867 CYTOPLASMIC (POTENTIAL).

CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 554 554 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 581 581 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 581 581 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 732 732 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 732 732 N-LINKED (GLCNAC. . .) (POTENTIAL).

CONFLICT 64 64 S -> N (IN REF. 2).

CONFLICT 656 668 668 P -> L (IN REF. 2).

CONFLICT 668 668 P -> L (IN REF. 2).

CONFLICT 844 844 G -> D (IN REF. 2).

SEQUENCE 867 AA; 97112 MW; D442F6372552B3C8 CRC64;
       DOMAIN 180 434
FT
                                             EXTRACELLULAR (POTENTIAL).
FT
SQ SEQUENCE 867 AA; 97112 MW; D442F6372552B3C8 CRC64;
  Query Match
                                    9.0%; Score 86.5; DB 1; Length 867;
  Best Local Similarity 22.7%; Pred. No. 2.6;
  Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps
Qу
              18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
                  Db
              126 LVGCFFCMCRC-----CNK-CGGEMHOROKONAPCRRKCLGLSLLVICLLMSLGIIY 176
Qу
              78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
                     Db
             177 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKOIDYVVEQYTNTKNKA 227
             130 ----DCIKS-----KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL- 172
QУ
                     228 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 280
Db
    173 ---SATEIEKSISA 183
QУ
                       :||:: ::|:
Db 281 LQDAATQLNTNLSS 294
RESULT 7
FAK2 MOUSE
ID FAK2 MOUSE
                         STANDARD; PRT; 1009 AA.
AC
       Q9QVP9;
DT
       28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
     Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
       2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
DE
       beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related
DE
       adhesion focal tyrosine kinase).
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GN
     PTK2B OR FAK2 OR PYK2 OR RAFTK.
OS
     Mus musculus (Mouse).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
     NCBI TaxID=10090;
RN
RP
     SEQUENCE FROM N.A.
RC
     TISSUE=Brain;
RX
     MEDLINE=96070905; PubMed=7499242;
RA
     Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S.,
RA
     Pasztor L.M., White R.A., Groopman J.E., Avraham H.;
RT
     "Identification and characterization of a novel related adhesion focal
RT
     tyrosine kinase (RAFTK) from megakaryocytes and brain.";
RL
     J. Biol. Chem. 270:27742-27751(1995).
RN
     [2]
RP
     PTPNS1 BINDING.
RX
    MEDLINE=99401000; PubMed=10469599;
RA
     Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E.,
     Schraven B., Neel B.G.;
RA
RT
     "SHPS-1 is a scaffold for assembling distinct adhesion-regulated
RT
    multi-protein complexes in macrophages.";
RL
     Curr. Biol. 9:927-930(1999).
RN
RP
    PHOSPHORYLATION OF TYR-402; TYR-580 AND TYR-881.
RX
    MEDLINE=21313779; PubMed=11420674;
RA
    Nakamura K., Yano H., Schaefer E., Sabe H.;
     "Different modes and qualities of tyrosine phosphorylation of Fak and
RT
RT
     Pyk2 during epithelial-mesenchymal transdifferentiation and cell
RT
     migration: analysis of specific phosphorylation events using
RT
     site-directed antibodies.";
RL
    Oncogene 20:2626-2635(2001).
RN
RP
     PHOSPHORYLATION OF TYR-402, AND INTERACTION WITH NEPHROCYSTIN.
RX
    MEDLINE=21396557; PubMed=11493697;
     Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
RA
RT
     "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers
RT
    phosphorylation of Pyk2.";
RL
    Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
CC
    -!- FUNCTION: Involved in calcium induced regulation of ion channel
         and activation of the map kinase signaling pathway. May represent
CC
CC
         an important signaling intermediate between neuropeptide activated
CC
         receptors or neurotransmitters that increase calcium flux and the
CC
         downstream signals that regulate neuronal activity. Interacts with
CC
         the SH2 domain of Grb2. May phosphorylate the voltage-gated
CC
         potassium channel protein Kv1.2. Its activation is highly
CC
         correlated with the stimulation of c-Jun N-terminal kinase
CC
         activity (By similarity).
CC
    -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC
         tyrosine phosphate.
CC
    -!- SUBUNIT: Interacts with Crk-associated substrate (Cas), PTPNS1,
CC
        Nephrocystin and GTPase regulator associated with FAK (Graf).
CC
    -!- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
CC
         induces the membrane-association of the kinase.
    -!- PTM: Phosphorylated on tyrosine residues in response to various
CC
         stimuli that elevate the intracellular calcium concentration, as
CC
CC
         well as by PKC activation. Recruitment by Nephrocystin to cell
CC
         matrix adhesions initiates Tyr-402 phosphorylation. In monocytes,
```

```
CC
        adherence to substrata is required for tyrosine phosphorylation
CC
        and kinase activation. Angiotensin II, thapsigargin and L-alpha-
CC
        lysophosphatidic acid (LPA) also induce autophosphorylation and
CC
        increase kinase activity (By similarity).
CC
    -!- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
CC
        subfamily.
    -!- SIMILARITY: Contains 1 FERM domain.
CC
    HSSP; P08631; 1AD5.
DR
DR
    MGD; MGI:104908; Ptk2b.
DR
    InterPro; IPR000299; Band 4.1.
    InterPro; IPR005189; Focal AT.
DR
    InterPro; IPR000719; Prot kinase.
DR
    InterPro; IPR001245; Tyr pkinase.
DR
    InterPro; IPR008266; Tyr_pkinase_AS.
DR
DR
    Pfam; PF03623; Focal AT; 1.
    Pfam; PF00069; pkinase; 1.
DR
DR
    PRINTS; PR00109; TYRKINASE.
DR
    ProDom; PD000001; Prot kinase; 1.
DR
    SMART; SM00295; B41; 1.
DR
    SMART; SM00219; TyrKc; 1.
DR
    PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR
    PROSITE; PS50011; PROTEIN KINASE DOM; 1.
    PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR
DR
    PROSITE; PS00660; FERM 1; FALSE NEG.
    PROSITE; PS00661; FERM 2; FALSE NEG.
DR
    PROSITE; PS50057; FERM 3; 1.
    Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation.
KW
FT
    DOMAIN
                39
                      359
                               FERM.
FT
    DOMAIN
               425
                      683
                               PROTEIN KINASE.
                    439
457
FT
    NP BIND
               431
                              ATP (BY SIMILARITY).
    BINDING
               457
                              ATP (BY SIMILARITY).
FT
FT
    ACT SITE
               549 549
                              BY SIMILARITY.
               701 767
831 869
FT
    DOMAIN
                              PRO-RICH.
    DOMAIN
                              PRO-RICH.
FT
                    1009
               868
FT
    DOMAIN
                               FOCAL ADHESION TARGETING (FAT).
                   402
579
    MOD RES
               402
FT
                               PHOSPHORYLATION.
FΤ
    MOD RES
               579
                               PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT
    MOD RES
               580
                    580
                               PHOSPHORYLATION.
    MOD RES
                               PHOSPHORYLATION.
FT
               881
                     881
SO
    SEQUENCE 1009 AA; 115821 MW; 963959FF56DF9605 CRC64;
 Query Match
                         8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 7.9;
          29; Conservative 13; Mismatches 34; Indels
                                                            32; Gaps
                                                                         4;
          88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
Qу
             |:
         249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDTKPTCLAEFKQI 305
Db
         139 DSDHCFPLPAME-----EGATILVTTKTND-----YCK 166
Qу
              | | | | : : | |:
         306 RSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR 353
Db
RESULT 8
FAK2 RAT
ID
    FAK2 RAT
                 STANDARD; PRT; 1009 AA.
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AС
     P70600; 088489; Q63201;
DΤ
     15-JUL-1998 (Rel. 36, Created)
DT
     15-JUL-1998 (Rel. 36, Last sequence update)
     10-OCT-2003 (Rel. 42, Last annotation update)
DT
DΕ
     Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
DE
     2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
DE
     beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK).
GN
     PTK2B OR FAK2 OR PYK2.
OS
     Rattus norvegicus (Rat).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX
     NCBI TaxID=10116;
RN
RP
     SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 310-334; 553-572;
RP
     672-687 AND 989-998.
RC
     TISSUE=Liver epithelium;
RX
     MEDLINE=97094711; PubMed=8939945;
RA
     Yu H., Li X., Marchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.L.,
RA
     Wilm M., Anderegg R.J., Graves L.M., Earp H.S.;
RT
     "Activation of a novel calcium-dependent protein-tyrosine kinase.
RT
     Correlation with c-Jun N-terminal kinase but not mitogen-activated
RT
     protein kinase activation.";
RL
     J. Biol. Chem. 271:29993-29998(1996).
RN
RP
     SEQUENCE FROM N.A. (ISOFORM 1).
RC
     STRAIN=Sprague-Dawley; TISSUE=Brain;
RX
     MEDLINE=95403356; PubMed=7673154;
     Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sasaki T.;
RA
RT
     "Cloning and characterization of cell adhesion kinase beta, a novel
RT
     protein-tyrosine kinase of the focal adhesion kinase subfamily.";
RL
     J. Biol. Chem. 270:21206-21219(1995).
RN
RP
     SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SUBCELLULAR LOCATION, AND FAT
RP
     DOMAIN.
RC
     TISSUE=Hippocampus;
RX
     MEDLINE=98311659; PubMed=9645946;
RA
     Xiong W.-C., Macklem M., Parsons J.T.;
RT
     "Expression and characterization of splice variants of PYK2, a focal
RT
     adhesion kinase-related protein.";
RL
     J. Cell Sci. 111:1981-1991(1998).
CC
     -!- FUNCTION: Involved in calcium induced regulation of ion channel
CC
         and activation of the map kinase signaling pathway. May represent
CC
         an important signaling intermediate between neuropeptide activated
CC
         receptors or neurotransmitters that increase calcium flux and the
CC
         downstream signals that regulate neuronal activity. Interacts with
CC
         the SH2 domain of Grb2. May phosphorylate the voltage-gated
CC
         potassium channel protein Kv1.2. Its activation is highly
CC
         correlated with the stimulation of c-Jun N-terminal kinase
CC
        activity.
CC
    -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
        tyrosine phosphate.
CC
CC
    -!- SUBUNIT: Interacts with PTPNS1 (By similarity). Isoform 1, but not
CC
         isoform 2, interacts with Crk-associated substrate (Cas),
CC
         Nephrocystin and GTPase regulator associated with FAK (Graf).
CC
    -!- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
```

induces the membrane-association of the kinase (By similarity).

Isoform 2 localizes to focal adhesions, but not isoforms 1 and 3.

CC

CC

```
CC
     -!- ALTERNATIVE PRODUCTS:
CC
        Event=Alternative splicing; Named isoforms=3;
CC
        Name=1;
          IsoId=P70600-1; Sequence=Displayed;
CC
CC
        Name=2; Synonyms=PRNK;
CC
          IsoId=P70600-2; Sequence=VSP 004982, VSP 004983;
CC
        Name=3; Synonyms=PYK2s;
CC
          IsoId=P70600-3; Sequence=VSP 004984;
     -!- TISSUE SPECIFICITY: Isoform 1 is expressed at high levels in the
CC
CC
        brain (hippocampus, cerebral cortex and olfactory bulb) and poorly
CC
        in the spleen and other tissues, whereas isoforms 2 and 3 are
CC
        expressed in the spleen and brain (highest in cerebellum).
CC
     -!- PTM: Phosphorylated on tyrosine residues in response to various
CC
        stimuli that elevate the intracellular calcium concentration, as
CC
        well as by PKC activation. Recruitment by Nephrocystin to cell
CC
        matrix adhesions initiates Tyr-402 phosphorylation (By
CC
        similarity). In monocytes, adherence to substrata is required for
CC
        tyrosine phosphorylation and kinase activation. Angiotensin II,
CC
        thapsigargin and L-alpha-lysophosphatidic acid (LPA) also induce
CC
        autophosphorylation and increase kinase activity.
CC
    -!- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
CC
        subfamily.
    -!- SIMILARITY: Contains 1 FERM domain.
CC
CC
    CC
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
CC
    use by non-profit institutions as long as its content is in no way
CC
    modified and this statement is not removed. Usage by and for commercial
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
    or send an email to license@isb-sib.ch).
CC
    ______
DR
    EMBL; U69109; AAC52895.1; -.
DR
    EMBL; D45854; BAA08290.1; -.
    EMBL; AF063890; AAC28340.1; -.
DR
DR
    PIR; A57434; A57434.
DR
    HSSP; P00523; 2PTK.
DR
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    InterPro; IPR005189; Focal AT.
DR
    InterPro; IPR000719; Prot kinase.
DR
    InterPro; IPR001245; Tyr pkinase.
    InterPro; IPR008266; Tyr pkinase AS.
DR
DR
    Pfam; PF03623; Focal AT; 1.
    Pfam; PF00069; pkinase; 1.
DR
DR
    PRINTS; PR00109; TYRKINASE.
DR
    ProDom; PD000001; Prot kinase; 1.
DR
    SMART; SM00295; B41; 1.
DR
    SMART; SM00219; TyrKc; 1.
    PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR
    PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR
DR
    PROSITE; PS50011; PROTEIN KINASE DOM; 1.
    PROSITE; PS00660; FERM 1; FALSE NEG.
DR
DR
    PROSITE; PS00661; FERM 2; FALSE NEG.
    PROSITE; PS50057; FERM 3; 1.
    Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation;
KW
KW
    Alternative splicing.
FT
    DOMAIN
             39
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                               FERM.
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425 683
431 439
457 457
                             PROTEIN KINASE.
FT
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     NP BIND
                                ATP (BY SIMILARITY).
FT
     BINDING
                                ATP (BY SIMILARITY).
     ACT SITE 549 549
FT
                                BY SIMILARITY.
FT
     DOMAIN
               701
                      767
                                 PRO-RICH.
               831
FT
     DOMAIN
                       869
                                 PRO-RICH.
                     1009
                868
FT
     DOMAIN
               968 1000 402 PHOSPHORILATION (AUTO-) (BY SIMILARITY).
579 579 PHOSPHORYLATION (BY SIMILARITY).
881 881 PHOSPHORYLATION (BY SIMILARITY).
1 771 Missing (in isoform 2).

/TITE-VSP 004982.
                                 FOCAL ADHESION TARGETING (FAT).
FT
     MOD RES
FT
    MOD RES
                                PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
     MOD RES
FT
     MOD_RES 881 881
VARSPLIC 1 771
FT
FT
FT
     VARSPLIC 772 780
FT
                                 NVFKRHSMR -> MGLIVLSSQ (in isoform 2).
FT
                                 /FTId=VSP 004983.
    VARSPLIC 739 780
FT
                                Missing (in isoform 3).
FT
                                 /FTId=VSP 004984.
    CONFLICT 205 205
FT
                                 E \rightarrow A (IN REF. 2).
               807 807
FT
     CONFLICT
                                 V \rightarrow F (IN REF. 3).
SQ
     SEQUENCE 1009 AA; 115784 MW; D435A475BCA49E9B CRC64;
  Query Match
                          8.5%; Score 82; DB 1; Length 1009;
  Best Local Similarity 26.9%; Pred. No. 7.9;
 Matches 29; Conservative 13; Mismatches 34; Indels
          88 EFKNTGSGLLGMANIDLEKSR----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
QУ
          Db
          249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDTKPTCLAEFKQI 305
Qу
          139 DSDHCFPLPAME-----EGATILVTTKTND-----YCK 166
              | | | | | :: | |: | |: | |:
Db
          306 RSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR 353
RESULT 9
FAK2 HUMAN
     FAK2 HUMAN
                STANDARD; PRT; 1009 AA.
    Q14289; Q13475; Q14290; Q16709;
    15-JUL-1998 (Rel. 36, Created)
DT
    15-JUL-1998 (Rel. 36, Last sequence update)
DТ
    10-OCT-2003 (Rel. 42, Last annotation update)
DE
    Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
DE
    2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
DE
    beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related
DE
    adhesion focal tyrosine kinase).
GN
    PTK2B OR FAK2 OR PYK2 OR RAFTK.
OS
    Homo sapiens (Human).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX
    NCBI TaxID=9606;
RN
    [1]
RP
    SEQUENCE FROM N.A. (ISOFORM 1).
RC
    TISSUE=Brain;
    MEDLINE=95379967; PubMed=7544443;
    Lev S., Moreno H., Martinez R., Canoll P., Peles E., Musacchio J.M.,
RA
    Plowman G.D., Rudy B., Schlessinger J.;
RA
     "Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation
RT
```

```
of ion channel and MAP kinase functions.";
RL
     Nature 376:737-745(1995).
RN
RP
     SEQUENCE FROM N.A. (ISOFORM 1).
RC
     TISSUE=Hippocampus;
RX
     MEDLINE=96435932; PubMed=8838818;
RA
     Herzog H., Nicholl J., Hort Y.J., Sutherland G.R., Shine J.;
RT
     "Molecular cloning and assignment of FAK2, a novel human focal
RT
     adhesion kinase, to 8p11.2-p22 by nonisotopic in situ hybridization.";
RL
     Genomics 32:484-486(1996).
RN
RP
     SEQUENCE FROM N.A. (ISOFORM 1).
RC
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RX
     MEDLINE=95403356; PubMed=7673154;
RA
     Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sasaki T.;
RT
     "Cloning and characterization of cell adhesion kinase beta, a novel
     protein-tyrosine kinase of the focal adhesion kinase subfamily.";
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RL
     J. Biol. Chem. 270:21206-21219(1995).
RN
RP
     SEQUENCE FROM N.A. (ISOFORM 1).
RX
     MEDLINE=96070905; PubMed=7499242;
     Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S.,
RA
RA
     Pasztor L.M., White R.A., Groopman J.E., Avraham H.;
RT
     "Identification and characterization of a novel related adhesion focal
     tyrosine kinase (RAFTK) from megakaryocytes and brain.";
RL
     J. Biol. Chem. 270:27742-27751(1995).
RN
     [5]
RΡ
     SEQUENCE FROM N.A. (ISOFORM 2).
RC
     TISSUE=Monocytes;
RX
     MEDLINE=98211954; PubMed=9545257;
RA
     Li X., Hunter D., Morris J., Haskill J.S., Earp H.S.;
RT
     "A calcium-dependent tyrosine kinase splice variant in human
RT
     monocytes. Activation by a two-stage process involving adherence and a
RT
     subsequent intracellular signal.";
RL
     J. Biol. Chem. 273:9361-9364(1998).
RN
     [6]
RP
     SEQUENCE FROM N.A.
RA
     Blechschmidt K., Jandrig B., Baumgart C., Dette M.D., Jahn N.,
RA
     Menzel U., Schilhabel M.B., Wen G., Taudien S., Rosenthal A.;
RL
     Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RN
RP
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RC
     TISSUE=Lymph;
RX
    MEDLINE=22388257; PubMed=12477932;
RA
     Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
     Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA
     Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA
    Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA
     Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
     Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA
     Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA
RA
     Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
     Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA
RA
     Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
    Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA
RA
     Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA
    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
```

```
RA
     Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
     Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA
RA
     Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA
     Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RТ
     "Generation and initial analysis of more than 15,000 full-length
RT
     human and mouse cDNA sequences.";
RL
     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP
     PHOSPHORYLATION OF TYR-402, MUTAGENESIS OF PRO-859, AND INTERACTION
RP
     WITH NEPHROCYSTIN.
RX
     MEDLINE=21396557; PubMed=11493697;
RA
     Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
RT
     "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers
RT
     phosphorylation of Pyk2.";
RL
     Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
CC
     -!- FUNCTION: Involved in calcium induced regulation of ion channel
         and activation of the map kinase signaling pathway. May represent
CC
CC
         an important signaling intermediate between neuropeptide activated
CC
         receptors or neurotransmitters that increase calcium flux and the
CC
         downstream signals that regulate neuronal activity. Interacts with
CC
         the SH2 domain of Grb2. May phosphorylate the voltage-gated
CC
         potassium channel protein Kv1.2. Its activation is highly
CC
         correlated with the stimulation of c-Jun N-terminal kinase
CC
     -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC
CC
         tyrosine phosphate.
CC
     -!- SUBUNIT: Interacts with Crk-associated substrate (Cas), PTPNS1 (By
CC
         similarity), Nephrocystin and GTPase regulator associated with FAK
CC
         (Graf).
CC
     -!- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
CC
         induces the membrane-association of the kinase.
CC
     -!- ALTERNATIVE PRODUCTS:
CC
         Event=Alternative splicing; Named isoforms=2;
CC
         Name=1;
CC
           IsoId=Q14289-1; Sequence=Displayed;
CC
        Name=2;
CC
          IsoId=Q14289-2; Sequence=VSP 004981;
CC
    -!- TISSUE SPECIFICITY: Most abundant in the brain, with highest
CC
        levels in amygdala and hippocampus. Low levels in kidney. Also
CC
         expressed in spleen and lymphocytes.
CC
     -!- PTM: Phosphorylated on tyrosine residues in response to various
CC
         stimuli that elevate the intracellular calcium concentration, as
CC
        well as by PKC activation. Recruitment by Nephrocystin to cell
CC
        matrix adhesions initiates Tyr-402 phosphorylation. In monocytes,
CC
         adherence to substrata is required for tyrosine phosphorylation
CC
         and kinase activation. Angiotensin II, thapsigargin and L-alpha-
CC
        lysophosphatidic acid (LPA) also induce autophosphorylation and
CC
        increase kinase activity (By similarity).
CC
    -!- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
CC
        subfamily.
     -!- SIMILARITY: Contains 1 FERM domain.
CC
CC
CC
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     the European Bioinformatics Institute. There are no restrictions on its
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     modified and this statement is not removed. Usage by and for commercial
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    or send an email to license@isb-sib.ch).
    CC
    EMBL; U33284; AAC50203.1; -.
DR
    EMBL; L49207; AAB47217.1; -.
DR
DR
    EMBL; D45853; BAA08289.1; -.
DR
    EMBL; U43522; AAC05330.1; -.
DR
    EMBL; S80542; AAB35701.1; -.
DR
    EMBL; AF311103; -; NOT ANNOTATED CDS.
    EMBL; BC042599; AAH42599.1; -.
DR
    PIR; S60248; S60248.
DR
    HSSP; P08631; 1AD5.
DR
    Genew; HGNC:9612; PTK2B.
DR
    MIM; 601212; -.
DR
    GO; GO:0005737; C:cytoplasm; TAS.
    GO; GO:0004717; F:focal adhesion kinase activity; TAS.
DR
    GO; GO:0004715; F:non-membrane spanning protein tyrosine kina. . .; TAS.
DR
DR
    GO; GO:0006915; P:apoptosis; TAS.
    GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR
DR
    GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR
    GO; GO:0006461; P:protein complex assembly; TAS.
DR
    GO; GO:0006950; P:response to stress; TAS.
DR
    GO; GO:0007172; P:signal complex formation; TAS.
    GO; GO:0007165; P:signal transduction; TAS.
    InterPro; IPR000299; Band 4.1.
DR
    InterPro; IPR005189; Focal AT.
DR
    InterPro; IPR000719; Prot_kinase.
DR
    InterPro; IPR001245; Tyr pkinase.
DR
    InterPro; IPR008266; Tyr_pkinase_AS.
DR
    Pfam; PF03623; Focal AT; 1.
DR
DR
    Pfam; PF00069; pkinase; 1.
DR
    PRINTS; PR00109; TYRKINASE.
    ProDom; PD000001; Prot_kinase; 1.
DR
    SMART; SM00295; B41; 1.
DR
    SMART; SM00219; TyrKc; 1.
DR
DR
    PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR
    PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR
    PROSITE; PS50011; PROTEIN KINASE DOM; 1.
    PROSITE; PS00660; FERM 1; FALSE NEG.
    PROSITE; PS00661; FERM 2; FALSE NEG.
DR
    PROSITE; PS50057; FERM 3; 1.
DR
KW
    Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation;
KW
    Alternative splicing.
FT
    DOMAIN
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                      359
                                FERM.
               425
FT
    DOMAIN
                      683
                               PROTEIN KINASE.
    NP BIND
               431
                    439
FT
                               ATP (BY SIMILARITY).
    BINDING
               457
                     457
                                ATP (BY SIMILARITY).
FΤ
                    549
    ACT SITE
               549
FT
                               BY SIMILARITY.
              702
                    767
FT
    DOMAIN
                                PRO-RICH.
FT
    DOMAIN
               831
                     869
                                PRO-RICH.
               868
                    1009
FT
    DOMAIN
                               FOCAL ADHESION TARGETING (FAT).
                    402
FT
    MOD RES
              402
                               PHOSPHORYLATION.
              579
                     579
FT
    MOD RES
                               PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
    MOD RES
              580
FT
                    580
                               PHOSPHORYLATION (BY SIMILARITY).
            881
739
                     881
FT
    MOD RES
                                PHOSPHORYLATION (BY SIMILARITY).
                    780
FT
    VARSPLIC
                               Missing (in isoform 2).
FT
                                /FTId=VSP 004981.
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FT
     MUTAGEN
                 859
                        859
                                  P->A: LOSS OF INTERACTION WITH
FT
                                  NEPHROCYSTIN.
FT
     CONFLICT
                 23
                        23
                                  A \rightarrow G (IN REF. 3).
FT
     CONFLICT
                 256
                        256
                                  G \rightarrow P (IN REF. 2).
FT
     CONFLICT
                 435
                                  F \rightarrow L (IN REF. 3).
                        435
FT
     CONFLICT
                 780
                        780
                                  R \rightarrow G (IN REF. 2).
SQ
     SEQUENCE
                1009 AA; 115874 MW; 420B21046274E7C2 CRC64;
  Query Match
                            8.2%; Score 79.5; DB 1; Length 1009;
  Best Local Similarity
                          32.1%; Pred. No. 13;
  Matches
            25; Conservative 9; Mismatches
                                                   29; Indels
                                                                 15; Gaps
QУ
           88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
              : | | | | | | | | | |
                                            :
Db
          249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
          139 DSDHCFPLPAMEEGATIL 156
Qу
               1 | | | | : |
Db
          306 RSIRCLPL---EEGQAVL 320
RESULT 10
T13X HUMAN
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                    STANDARD;
                                   PRT;
                                          293 AA.
AC
     014836;
DT
     28-FEB-2003 (Rel. 41, Created)
DT
     28-FEB-2003 (Rel. 41, Last sequence update)
DT
     10-OCT-2003 (Rel. 42, Last annotation update)
DE
     Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE
     activator and CAML interactor).
     TNFRSF13B OR TACI.
GN
OS
     Homo sapiens (Human).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC
OX
     NCBI TaxID=9606;
RN
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RP
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RC
     TISSUE=B-cell;
RX
     MEDLINE=97458245; PubMed=9311921;
RA
     von Buelow G.-U., Bram R.J.;
RT
     "NF-AT activation induced by a CAML-interacting member of the tumor
RT
     necrosis factor receptor superfamily.";
RL
     Science 278:138-141(1997).
RN
     [2]
RP
     SEQUENCE FROM N.A.
RC
     TISSUE=Blood;
    MEDLINE=22388257; PubMed=12477932;
RX
RA
     Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
     Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA
     Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA
RA
     Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA
     Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
     Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA
RA
     Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
     Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA
     Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA
     Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA
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RA
     Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA
     Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA
     Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA
     Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
     Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA
     Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA
RA
     Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT
     "Generation and initial analysis of more than 15,000 full-length
RT
     human and mouse cDNA sequences.";
RL
     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
RP
     FUNCTION.
RX
    MEDLINE=20519647; PubMed=10956646;
     Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA
RA
     Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., LaFleur D.,
RA
     Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA
     Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT
     "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT
     high affinity receptor for TNF family members APRIL and BLyS.";
RL
     J. Biol. Chem. 275:35478-35485(2000).
RN
     [4]
RP
     FUNCTION.
RX
    MEDLINE=21170294; PubMed=10973284;
RA
    Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA
    McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA
     Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT
     "APRIL and TALL-I and receptors BCMA and TACI: system for regulating
RT
    humoral immunity.";
RL
    Nat. Immunol. 1:252-256(2000).
RN
    INTERACTION WITH TRAF2 AND TRAF5.
RP
RX
    MEDLINE=20341628; PubMed=10880535;
RA
    Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
    Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
RA
RA
    Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
RA
    Meng S.Y., Boyle W.J., Hsu H.;
RТ
    "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT
    factor family member involved in B cell regulation.";
RL
    J. Exp. Med. 192:137-143(2000).
CC
    -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
CC
        that binds both ligands with similar high affinity. Mediates
CC
        calcineurin-dependent activation of NF-AT, as well as activation
CC
        of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC
        cell function and the regulation of humoral immunity.
CC
    -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC
        domain of CAMLG with its C-terminus.
CC
    -!- SUBCELLULAR LOCATION: Type III membrane protein.
CC
    -!- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC
        intestine and peripheral blood leukocytes. Expressed in resting B-
CC
        cells and activated T-cells, but not in resting T-cells.
CC
    -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
    -!- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
CC
CC
    CC
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         or send an email to license@isb-sib.ch).
CC
         EMBL; AF023614; AAC51790.1; -.
DR
DR
         EMBL; BC028072; AAH28072.1; -.
DR
         Genew; HGNC:18153; TNFRSF13B.
         MIM; 604907; -.
DR
DR
         GO; GO:0005887; C:integral to plasma membrane; TAS.
         GO; GO:0004872; F:receptor activity; TAS.
         GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
DR
         InterPro; IPR001368; TNFR c6.
DR
         PROSITE; PS00652; TNFR NGFR 1; 1.
         PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.
KW
         Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
KW
         Repeat.
FT
         DOMAIN
                                        165
                                                          EXTRACELLULAR (POTENTIAL).
FT
         TRANSMEM 166 186
                                                          SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT
                                                            (POTENTIAL).
       (POTENTIAL).

DOMAIN 187 293 CYTOPLASMIC (POTENTIAL).

REPEAT 33 67 TNFR-CYS 1.

REPEAT 70 104 TNFR-CYS 2.

DISULFID 34 47 BY SIMILARITY.

DISULFID 50 62 BY SIMILARITY.

DISULFID 54 66 BY SIMILARITY.

DISULFID 71 86 BY SIMILARITY.

DISULFID 71 86 BY SIMILARITY.

DISULFID 89 100 BY SIMILARITY.

DISULFID 89 100 BY SIMILARITY.

DISULFID 93 104 BY SIMILARITY.

CARBOHYD 128 128 N-LINKED (GLCNAC. . . ) (FROME AND ADMINISTRATION AND A
FT
FT
FT
FT
FT
       DISULFID
FT
       DISULFID
      DISULFID
FT
      DISULFID
FT
FT
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL). FT CONFLICT 251 251 P \rightarrow L (IN REF. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
   Query Match
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                                                                                                                                       10;
Qу
                   8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
                       34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
Db
                   66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
QУ
                              Db
                  93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
                 108 ---RTGDEIILPRG------KVD 139
QУ
                                                        |: :|:|: |
                              : |:: |
Db
                 152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
                140 SDHCFPLPAMEEGATILVTTKTNDYC 165
Qy
                         Db
                 210 QDH----AMEAGSPVSTSPEPVETC 230
RESULT 11
MJK2 METJA
ID MJK2 METJA STANDARD; PRT; 343 AA.
AC Q58752;
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DT
     01-NOV-1997 (Rel. 35, Created)
DT
     01-NOV-1997 (Rel. 35, Last sequence update)
DT
     15-MAR-2004 (Rel. 43, Last annotation update)
     Probable potassium channel protein 2 (MjK2).
DΕ
GN
     MJ1357.
OS
     Methanococcus jannaschii.
     Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC
     Methanocaldococcaceae; Methanocaldococcus.
OC
OX
     NCBI TaxID=2190;
RN
RP
     SEQUENCE FROM N.A.
RC
     STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX
     MEDLINE=96337999; PubMed=8688087;
     Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA
     Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA
RA
     Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
     Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA
RA
     Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA
     Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
     Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA
RA
     Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
     "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT
RT
     jannaschii.";
RL
     Science 273:1058-1073(1996).
RN
     [2]
RP
     FUNCTION.
     STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RC
RX
    MEDLINE=22744766; PubMed=12860407;
RA
     Hellmer J., Zeilinger C.;
RT
     "MjK1, a K+ channel from M. jannaschii, mediates K+ uptake and K+
RT
     sensitivity in E. coli.";
RL
     FEBS Lett. 547:165-169(2003).
CC
    -!- FUNCTION: Probable potassium channel protein.
CC
    -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC
    -!- SIMILARITY: Contains 1 trkA/RCK domain.
CC
     ______
CC
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CC
     DR
    EMBL; U67575; AAB99365.1; -.
DR
    PIR; D64469; D64469.
    HSSP; Q54397; 1BL8.
DR
DR
    TIGR; MJ1357; -.
DR
    InterPro; IPR001622; K+channel pore.
DR
    InterPro; IPR003148; TrkA N.
DR
    InterPro; IPR006037; TrkAC.
DR
    Pfam; PF02080; TrkA-C; 1.
DR
    Pfam; PF02254; TrkA-N; 1.
    Transport; Ion transport; Ionic channel; Potassium; Potassium;
KW
    Potassium transport; Transmembrane; Complete proteome.
                        7
FT
    DOMAIN
                  1
                               CYTOPLASMIC (POTENTIAL).
                        28
FT
    TRANSMEM
                  8
                               POTENTIAL.
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61
FT
     DOMAIN
                  29
                                  EXTRACELLULAR (POTENTIAL).
                  62
FT
     TRANSMEM
                       82
                                 POTENTIAL.
FT
     DOMAIN
                  83 343
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     SEQUENCE 343 AA; 38883 MW; 61231B0C001B54C4 CRC64;
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  Query Match
  Best Local Similarity
          39; Conservative 35; Mismatches 66; Indels
  Matches
                                                                51; Gaps
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Qу
              : | | : | : |
                                   : | | : : : | : : : | : : : |
           32 DYFTALYFSVI----TITTTGYGDFTPKTFLGRTLTVVYLCVGVGIVMYLFSL 80
Db
Qy
           72 VLMFL-----LRKISS--EPLKDEFKNTGSGLLGMA----NIDLEKSRTGD 111
                            1:1: : : | | | : | | | | | |
Db
           81 IAEFIVEGKFEEFVRLKKMKNKIKTLKDHYIICGYGRLGKVVGEKFIEENIPFIAIDINE 140
QУ
          112 EII-----LPRGLEYTVEECTCEDCIKSKPKV------DSDHCF-PLPAMEEG 152
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                       1
                                                          |:|: | | | |
Db
          141 DVLKEEYEKYPDKFLYIVGDAKKEEVLK-KAKIDKAKGLIATLPSDADNVFLTLTARELN 199
Qу
         153 ATILVTTKTND 163
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Db
          200 PNILITAKADE 210
RESULT 12
T13X MOUSE
ID
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                                  PRT; 249 AA.
AC
     Q9ET35; Q9DBZ3;
DT
     28-FEB-2003 (Rel. 41, Created)
DT
     28-FEB-2003 (Rel. 41, Last sequence update)
     28-FEB-2003 (Rel. 41, Last annotation update)
DF.
     Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE
     activator and CAML interactor).
GN
    TNFRSF13B OR TACI.
OS
    Mus musculus (Mouse).
OC
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX
    NCBI TaxID=10090;
RN
    [1]
RΡ
    SEQUENCE FROM N.A.
RC
     TISSUE=Spleen;
RX
    MEDLINE=21177254; PubMed=10881172;
RA
    Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A.,
RA
    Dixit V.M.;
RT
    "Identification of a receptor for BLyS demonstrates a crucial role in
RT
    humoral immunity.";
RL
    Nat. Immunol. 1:37-41(2000).
RN
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=C57BL/6J; TISSUE=Lung;
RX
    MEDLINE=21085660; PubMed=11217851;
    Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
    Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA
RA
    Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
    Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA
```

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RA
     Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA
     Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA
     Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA
     Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA
     Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA
     Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA
     Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA
     Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA
     Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA
     Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA
     Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
     Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA
     Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA
RA
     Hayashizaki Y.;
RT
     "Functional annotation of a full-length mouse cDNA collection.";
RL
     Nature 409:685-690(2001).
RN
RP
     FUNCTION.
RX
    MEDLINE=20341628; PubMed=10880535;
RA
    Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA
    Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
RA
    Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
RA
    Meng S.-Y., Boyle W.J., Hsu H.;
RT
     "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT
     factor family member involved in B cell regulation.";
RL
     J. Exp. Med. 192:137-143(2000).
RN
     [4]
RP
    FUNCTION.
RX
    MEDLINE=21322748; PubMed=11429548;
RA
    Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
RA
    Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
RT
     "TACI-ligand interactions are required for T cell activation and
RT
    collagen-induced arthritis in mice.";
RL
    Nat. Immunol. 2:632-637(2001).
    -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
CC
        that binds both ligands with similar high affinity. Mediates
CC
CC
        calcineurin-dependent activation of NF-AT, as well as activation
CC
        of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC
        cell function and the regulation of humoral immunity (By
CC
        similarity).
CC
    -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC
        domain of CAMLG with its C-terminus (By similarity).
CC
    -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC
    -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC
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CC
    EMBL; AF257673; AAG00081.1; -.
DR
DR
    EMBL; AK004668; BAB23457.1;
DR
    MGD; MGI:1889411; Tnfrsf13b.
DR
    GO; GO:0005887; C:integral to plasma membrane; IDA.
```

```
GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.
      InterPro; IPR001368; TNFR c6.
DR
DR
      PROSITE; PS00652; TNFR NGFR 1; FALSE NEG.
DR
      PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.
KW
      Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
FT
      DOMAIN
                   1 128
                                        EXTRACELLULAR (POTENTIAL).
      TRANSMEM
FT
                    129 149
                                        SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT
                                        (POTENTIAL).

        DOMAIN
        150
        249

        REPEAT
        5
        38
        TNFR-CYS 1.

        REPEAT
        42
        76
        TNFR-CYS 2.

        DISULFID
        6
        19
        BY SIMILARITY.

        DISULFID
        22
        34
        BY SIMILARITY.

        DISULFID
        26
        38
        BY SIMILARITY.

        DISULFID
        43
        58
        BY SIMILARITY.

        BY SIMILARITY.
        BY SIMILARITY.

                                     CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
FT
FT
FT
FT
FT
FT
FT
     DISULFID 61 72 BY SIMILARITY.
DISULFID 65 76 BY SIMILARITY.
CONFLICT 137 137 I -> F (IN REF. 2).
FT
FT
FΤ
     SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;
SO
  Query Match
                               8.0%; Score 77; DB 1; Length 249;
  Best Local Similarity 21.7%; Pred. No. 5.2;
  Matches 43; Conservative 21; Mismatches 70; Indels 64; Gaps 11;
Qу
             10 QNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCN---ASVTN-----SVKGTN 53
                Db
             47 QGRYYDHLLGACVSCDSTCTQH--PQQCAHFCEKRPRSQANLQPELGRPQAGEVEVRSDN 104
             54 A-----ILWTCLGLSLIISLAVFVL---MFLLRKISSEPLKDEFKN 91
Qy
                                        1: ||: | |:: || |: || :
Db
            105 SGRHQGSEHGPGLRLSSDQLTLYCTLGVCLCAIFCCFLVALASFLRRR--GEPLPSQPAG 162
           92 TGSGLLGMANIDLEKSRTGDEIIL-PRGLEYTVEECTCEDCI-----KSKPKVDSDH 142
Qу
                          163 PRGSQANSPHAHRPVTEACDEVTASPQPVE-----TCSFCFPERSSPTQESAPRSLGIH 216
Db
           143 CF----PLPAMEEGATI 155
Qу
                1 11:
Db
           217 GFAGTAAPQPCMR--ATV 232
RESULT 13
CI84 NEUCR
ID
     CI84 NEUCR
                     STANDARD; PRT; 748 AA.
AC
     042637;
DT
     10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
     Complex I intermediate-associated protein 84, mitochondrial precursor.
_{
m DE}
GN
     CIA84.
OS
     Neurospora crassa.
OC
    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
     Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
     NCBI TaxID=5141;
OX
RN
     [1]
RP
     SEQUENCE FROM N.A.
RX
     MEDLINE=98443243; PubMed=9769214;
```

DR

```
Kueffner R., Rohr A., Schmiede A., Kruell C., Schulte U.;
RA
RT
     "Involvement of two novel chaperones in the assembly of mitochondrial
RT
    NADH:ubiquinone oxidoreductase (complex 1).";
RL
     J. Mol. Biol. 283:409-417(1998).
CC
    -!- FUNCTION: Chaperone protein involved in the assembly of the
CC
        mitochondrial NADH: ubiquinone oxidoreductase complex (complex I).
CC
    -!- SUBCELLULAR LOCATION: Mitochondrial.
CC
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    ______
CC
DR
    EMBL; AJ001712; CAA04945.1; -.
DR
    PIR; T47250; T47250.
    InterPro; IPR008941; TPR-like.
DR
KW
    Chaperone; Mitochondrion; Transit peptide.
FT
    TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
FT
    CHAIN
                21
                     748
                             COMPLEX I INTERMEDIATE-ASSOCIATED
FT
                              PROTEIN 84.
SQ
    SEQUENCE 748 AA; 86342 MW; 8B2D80E98E8CDC73 CRC64;
  Query Match
                       7.9%; Score 76; DB 1; Length 748;
  Best Local Similarity 25.5%; Pred. No. 21;
         27; Conservative 20; Mismatches 49; Indels 10; Gaps
          82 SEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSD 141
Qу
            Db
         266 SKPIHSGFSPTGETLLELVRSSRRSSQKWNEWLLP-----VFEQVVQDKFAKKGSLDAF 319
         142 HCFPLPAMEEG----ATILVTTKTNDYCKSLPAALSATEIEKSISA 183
Qу
              Db
         320 LQWSVLALDKGPDGIKTYLQTMASGDFYQSHEVKVDATTINRLMQA 365
RESULT 14
YCSB SCHPO
ID
    YCSB SCHPO
                 STANDARD; PRT; 638 AA.
AC
    074910;
DT
    16-OCT-2001 (Rel. 40, Created)
DΤ
    16-OCT-2001 (Rel. 40, Last sequence update)
DТ
    28-FEB-2003 (Rel. 41, Last annotation update)
    Hypothetical WD-repeat protein C613.12c in chromosome III.
    SPCC613.12C.
GN
OS
    Schizosaccharomyces pombe (Fission yeast).
OC
    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC
    Schizosaccharomycetales; Schizosaccharomycetaceae;
OC
    Schizosaccharomyces.
OX
    NCBI TaxID=4896;
RN
    [1]
RP
    SEQUENCE FROM N.A.
RC
    STRAIN=972;
RX
    MEDLINE=21848401; PubMed=11859360;
RA
    Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
```

```
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA
     Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA
RA
     Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA
     Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA
     Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA
     James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA
     Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA
     Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
     Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA
RA
     Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
     Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA
RA
     Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA
     Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
     Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA
RA
     Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
     Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA
     Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA
     Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA
RA
     Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA
     Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA
     Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA
     Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA
     Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
     "The genome sequence of Schizosaccharomyces pombe.";
RT
     Nature 415:871-880(2002).
RL
CC
     -!- SIMILARITY: Contains 4 WD repeats.
CC
     CC
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DR
     EMBL; AL031644; CAA21064.1; -.
     PIR; T41478; T41478.
DR
DR
     GeneDB SPombe; SPCC613.12c; -.
DR
     InterPro; IPR001680; WD40.
DR
     Pfam; PF00400; WD40; 4.
DR
     PRINTS; PR00320; GPROTEINBRPT.
DR
     SMART; SM00320; WD40; 5.
DR
     PROSITE; PS00678; WD REPEATS 1; 2.
DR
     PROSITE; PS50082; WD REPEATS_2; 2.
DR
     PROSITE; PS50294; WD REPEATS REGION; 1.
ΚW
     Hypothetical protein; Repeat; WD repeat.
FT
     REPEAT
                297
                       336
                                 WD 1.
FT
     REPEAT
                486
                       525
                                 WD 2.
FT
     REPEAT
                544
                       583
                                 WD 3.
FT
     REPEAT
                587
                       626
                                 WD 4.
SO
     SEQUENCE
               638 AA; 71536 MW; 6CD360D8748AAF98 CRC64;
 Query Match
                          7.8%; Score 75.5; DB 1; Length 638;
 Best Local Similarity
                         22.7%; Pred. No. 20;
           44; Conservative 20; Mismatches
 Matches
                                                 61; Indels
                                                               69;
                                                                            7;
                                                                   Gaps
Qу
```

```
1:1 1:11
                                  | |: :: | | ::|
                                                           | | |::: |
Db
           42 EIYDPFYRAELPCP-----KPSLSISKHSIAKVPSNVNKR-----LELQLLLTSGTF 88
           72 VLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEEC---- 126
Qу
             89 L-----PNSRPYLSERVRKHTHL-----LSNSITGDDKPSLIHVDFTPEECFILQE 134
Db
          127 -----TCEDCIKSKPKVDSDHCFPLPAMEEGATILVT 158
Qу
                                          Db
          135 AKLKFGPVNSVQFNDAYSTHISPKLPGRAYEDC----QKFEIDNPSLSPVDKHGAIILRT 190
          159 TKTN-----DYCKS 167
Qy
              1 1
                      11 11
Db
          191 YKKNKKLLPDYLKS 204
RESULT 15
SRK6 BRAOL
ID
     SRK6 BRAOL
                   STANDARD;
                                PRT;
                                      849 AA.
AC
     Q09092;
DT
     01-FEB-1995 (Rel. 31, Created)
     01-FEB-1995 (Rel. 31, Last sequence update)
DT
ÐΤ
     15-MAR-2004 (Rel. 43, Last annotation update)
     Putative serine/threonine kinase receptor precursor (EC 2.7.1.37)
DE
     (S-receptor kinase) (SRK).
GN
     SRK6.
OS
     Brassica oleracea (Cauliflower).
OC
     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC
     Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC
     eurosids II; Brassicales; Brassicaceae; Brassica.
OX
    NCBI TaxID=3712;
RN
    T11
RP
    SEQUENCE FROM N.A.
     STRAIN=CV. S6S6; TISSUE=Stigma;
RC
    MEDLINE=92020942; PubMed=1681543;
RX
RA
     Stein J.C., Howlett B., Boyes D.C., Nasrallah M.E.;
RТ
    "Molecular cloning of a putative receptor protein kinase gene encoded
RT
    at the self-incompatibility locus of Brassica oleracea.";
RL
    Proc. Natl. Acad. Sci. U.S.A. 88:8816-8820(1991).
CC
    -!- FUNCTION: Involved in sporophytic self-incompatibility system
CC
        (the inability of flowering plants to achieve self-
CC
        fertilization), probably acting in combination with S-locus-
CC
        specific glycoproteins. Interaction with a ligand in the
CC
        extracellular domain triggers the protein kinase activity of the
CC
        cytoplasmic domain.
    -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC
    -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC
    -!- TISSUE SPECIFICITY: Predominantly in the pistil and anther.
CC
    -!- POLYMORPHISM: There are a number of different S alleles in
CC
CC
        B.oleracea, possibly providing the recognition specificity.
CC
    -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
    -!- SIMILARITY: Contains 1 bulb-type lectin domain.
CC
    -!- SIMILARITY: Contains 1 PAN domain.
CC
CC
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      ______
     EMBL; M76647; AAA33000.1; ALT TERM.
DR
DR
     InterPro; IPR001480; B lectin.
     InterPro; IPR003609; Pan app.
DR
DR
     InterPro; IPR000719; Prot kinase.
     InterPro; IPR008271; Ser thr pkin AS.
DR
     InterPro; IPR000858; Slocus glycop.
DR
     Pfam; PF01453; Agglutinin; 1.
DR
     Pfam; PF00069; pkinase; 1.
DR
     Pfam; PF00954; S locus_glycop; 1.
DR
     ProDom; PD000001; Prot kinase; 1.
DR
     SMART; SM00108; B lectin; 1.
     SMART; SM00473; PAN AP; 1.
DR
     PROSITE; PS50927; BULB LECTIN; 1.
     PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR
DR
     PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR
     PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW
     Transferase; Serine/threonine-protein kinase; Signal; ATP-binding;
KW
     Transmembrane; Receptor; Glycoprotein; Self-incompatibility.
FT
     SIGNAL
                   1
                         32
                                    POTENTIAL.
FT
     CHAIN
                   33
                         849
                                    PUTATIVE SERINE/THREONINE KINASE
FT
                                    RECEPTOR.
     DOMAIN 33 446
TRANSMEM 447 466
DOMAIN 467 849
FT
                                  EXTRACELLULAR (POTENTIAL).
FT
                                   POTENTIAL.
    DOMAIN 467 849

DOMAIN 35 155

BULB-TYPE LECTIN.

DOMAIN 528 779

PROTEIN KINASE.

NP_BIND 534 542

ATP (BY SIMILARITY).

BINDING 556 556

ATP (BY SIMILARITY).

ACT_SITE 653 653

BY SIMILARITY.

CARBOHYD 47 47

N-LINKED (GLCNAC. . ) (POTENTIAL).

CARBOHYD 120

CARBOHYD 196 196

N-LINKED (GLCNAC. . ) (POTENTIAL).

CARBOHYD 260 260

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).
FT
FT
FT
    DOMAIN
FT
    NP BIND
FT
    BINDING
FT
FT
FT
FT
FT
FT
FT
    CARBOHYD
                 389
                        389
                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
                 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
     CARBOHYD
FT
SO
   SEQUENCE
                849 AA; 97231 MW; 7E156059EDDF4370 CRC64;
  Query Match
                           7.8%; Score 75; DB 1; Length 849;
  Best Local Similarity 17.6%; Pred. No. 30;
  Matches 33; Conservative 30; Mismatches
                                                   50; Indels 74; Gaps
                                                                                 7;
Qу
           24 CQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWT----- 58
              Db
          380 CKKRCISD---CNCTAFANADIRNG--GSGCVIWTERLEDIRNYATDAIDGQDLYVRLAA 434
          59 -----CLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
Qy
                            435 ADIAKKRNASGKIISLTVGVSVLLLLIMFCL-----WKRKQKRAKASAISIANTQRNQ 487
Db
          107 SRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCF----PLPAMEEGATILVTTKT 161
Qy
              : : | : : |
```

Db 488 NLPMNEMVL------SSKREFSGEYKFEELELPLIEME---TVVKATEN 527

Qy 162 NDYCKSL 168

| | |
Db 528 FSSCNKL 534

Search completed: April 19, 2004, 13:21:30
Job time : 9.57202 secs